

SEQUENCE LISTING

5 <110> SunGene GmbH Co. KGaA

10 <120> Method for the production of Astaxanthin in flowers of plants

<130> PF 53862

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<160> 172

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<170> Patent in version 3.1

25 <210> 1

<211> 1771

<212> DNA

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<213> Haematococcus pluvialis

35 <220>

<221> CDS

<222> (166) .. (1155)

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35	ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc	513
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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
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Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
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Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
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Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
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Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
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Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
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Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
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Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
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Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

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His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

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Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
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Val Val, Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
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Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
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Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
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Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
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Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
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<222> (168) .. (1130)

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 Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
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20 agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc 272
 Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
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25 gag tgc tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct 320
 Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
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cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc 368
 Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
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30 acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg 416
 Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
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35 aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc 464
 Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
 85 90 95

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 Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp
 120 125 130

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	Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe	
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	gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg	800
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	Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn	
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	Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu	
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30	Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala	
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	gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca	992
	Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala	
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	tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg	1040
	Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp	
	280 285 290	
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	Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys	
	295 300 305	
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Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
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 Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
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10 Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
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Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
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25 Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
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30 Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
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35 Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
 180 185 190

40 Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
 195 200 205

45 Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
 210 215 220

11

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
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5 Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
 245 250 255

10 Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
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15 Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
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Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
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10	gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
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15	aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
	Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
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20	cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
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25	gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
	Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
	85 90 95	
30	cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
	Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
	100 105 110	
35	gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
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40	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
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	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
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	Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp				
10		85		90	95
	Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr				
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15	Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala				
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20	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro				
		130		135	140
	Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr				
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	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe				
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	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro				
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35	Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu				
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40	Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His				
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Thr Ala

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15

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ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212

Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp

40

25

30

35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260

Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr

40

45

50

45

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10	gcg ctg tgg ctc tat gcg ggg ttc tgg tgg ccc aag ctg atc gcc aag	404
	Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys	
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	Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr	
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	Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr	
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	Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg	
	185 190 195	
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	200 205 210	
50	ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg	788
	Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp	
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15	Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala 50 55 60		
20	His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn 65 70 75 80		
25	Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp 85 90 95		
30	Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr 100 105 110		
35	Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly 115 120 125		
40	Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro 130 135 140		
45	Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr 145 150 155 160		
	Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe 165 170 175		
	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro 180 185 190		

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205
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Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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 45 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His

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	Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala			
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	gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288		
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	Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala			
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	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro			
	130	135	140	
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	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe			
	165	170	175	
	gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576		
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	180	185	190	
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 Thr Ala

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 20 <213> Paracoccus marcusii

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 35 40 45

40 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

45 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

5 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

10 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

15 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

20 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

25 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

30 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

35 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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 Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
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 30 gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg 144
 Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
 35 40 45
 ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac 192
 35 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
 50 55 60
 gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag 240
 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
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 tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg 288
 Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
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	Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln	
	115 120 125	
10	ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt	432
	Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe	
	130 135 140	
15	aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg	480
	Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp	
	145 150 155 160	
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	Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala	
	165 170 175	
	ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat	576
	Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn	
	180 185 190	
25	gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt	624
	Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys	
	195 200 205	
30	tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg	672
	Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met	
	210 215 220	
35	atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga	720
	Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly	
	225 230 235 240	
40	ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa	768
	Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln	
	245 250 255	
	ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa	816
	Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu	
	260 265 270	
45	aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg	864

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	Ala	Lys	Lys	Gly	Val	Ile	Ser	Asn	Ile	Asp	Ala	Arg	Arg	Leu	Phe	Leu	
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10	caa	ttg	gtg	gaa	ccg	ggg	gcc	cta	gcc	aag	gtg	aat	caa	aac	cta	ggg	960
	Gln	Leu	Val	Glu	Pro	Gly	Ala	Leu	Ala	Lys	Val	Asn	Gln	Asn	Leu	Gly	
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15	gaa	cga	ctg	gaa	cgg	cgc	act	gtg	aac	aat	aac	gaa	gcc	att	tta	aaa	1008
	Glu	Arg	Leu	Glu	Arg	Arg	Thr	Val	Asn	Asn	Asn	Glu	Ala	Ile	Leu	Lys	
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20	atc	gat	tgt	gcc	ctc	tcc	ggg	tta	ccc	cac	ttc	act	gcc	atg	gcc	ggg	1056
	Ile	Asp	Cys	Ala	Leu	Ser	Gly	Leu	Pro	His	Phe	Thr	Ala	Met	Ala	Gly	
			340					345					350				
25	ccg	gag	gat	cta	acg	gga	act	att	ttg	att	gcc	gac	tcg	gta	cgc	cat	1104
	Pro	Glu	Asp	Leu	Thr	Gly	Thr	Ile	Leu	Ile	Ala	Asp	Ser	Val	Arg	His	
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30	gtc	gag	gaa	gcc	cac	gcc	ctc	att	gcc	ttg	ggg	caa	att	ccc	gat	gct	1152
	Val	Glu	Glu	Ala	His	Ala	Leu	Ile	Ala	Leu	Gly	Gln	Ile	Pro	Asp	Ala	
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40	gcc	ccc	cct	ggg	cag	cac	acc	ctc	tgg	atc	gaa	ttt	ttt	gcc	ccc	tac	1248
	Ala	Pro	Pro	Gly	Gln	His	Thr	Leu	Trp	Ile	Glu	Phe	Phe	Ala	Pro	Tyr	
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45	cgc	atc	gcc	ggg	ttg	gaa	ggg	aca	ggg	tta	atg	ggc	aca	ggg	tgg	acc	1296
	Arg	Ile	Ala	Gly	Leu	Glu	Gly	Thr	Gly	Leu	Met	Gly	Thr	Gly	Trp	Thr	
			420					425					430				
50	gat	gag	tta	aag	gaa	aaa	gtg	gcg	gat	cgg	gtg	att	gat	aaa	tta	acg	1344
	Asp	Glu	Leu	Lys	Glu	Lys	Val	Ala	Asp	Arg	Val	Ile	Asp	Lys	Leu	Thr	
		435					440					445					
55	gac	tat	gcc	cct	aac	cta	aaa	tct	ctg	atc	att	ggg	cgc	cga	gtg	gaa	1392
	Asp	Tyr	Ala	Pro	Asn	Leu	Lys	Ser	Leu	Ile	Ile	Gly	Arg	Arg	Val	Glu	

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	Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val			
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	tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta			1488
	Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu			
		485	490	495
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	ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca			1536
	Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr			
		500	505	510
15				
	ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga			1584
	Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg			
		515	520	525
	aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa			1629
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	Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met			
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Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
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Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 65 70 75 80

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Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
 85 90 95

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Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
 100 105 110

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Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
 115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
 130 135 140

25

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
 145 150 155 160

30

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
 165 170 175

35

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
 180 185 190

40

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
 195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
 210 215 220

45

Met Met, Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
 225 230 235 240

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Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
 245 250 255

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Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
 260 265 270

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Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
 275 280 285

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Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
 290 295 300

25

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
 305 310 315 320

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Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
 325 330 335

35

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
 340 345 350

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Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
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Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
 370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
 385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
 405 410 415

5 Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
 420 425 430

10 Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
 435 440 445

15 Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

20 Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
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 20 25 30

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ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192
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30 acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240
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 65 70 75 80

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	Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
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	Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
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10	Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu	
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	Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr	
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	ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccg ttc gcc gat	624
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	Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp	
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Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

25 Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

30 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

35 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

40 Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

45 Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu

165

170

175

5 Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
180 185 190

10 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
195 200 205

15 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
210 215 220

20 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
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 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
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 50 55 60
 20 atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240
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 65 70 75 80
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 85 90 95
 ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
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 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125
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 tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg 432
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140
 tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480
 40 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160
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 45 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu

PF :

35

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5	180	185	190	
	caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt			624
	Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly			
	195	200	205	
10	ggg tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt			672
	Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe			
	210	215	220	
15	tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac			720
	Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His			
	225	230	235	240
	gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata			768
20	Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile			
	245	250	255	
	tct tta taa			777
	Ser Leu			
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	Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe			
45	20	25	30	

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45
 5
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60
 10
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80
 15
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95
 20
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125
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 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140
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 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160
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 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175
 40
 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190
 45
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

Gly Tyr, Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

5

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
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Ser Leu

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ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 45 20 25 30

	tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc	143
	Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala	
	35 40 45	
5	cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc t'cg	191
	Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser	
	50 55 60	
10	tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga	239
	Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly	
	65 70 75	
	acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca	287
15	Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala	
	80 85 90 95	
	ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa	335
20	Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys	
	100 105 110	
	cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc	383
	Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly	
	115 120 125	
25	gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac	431
	Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His	
	130 135 140	
30	atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc	479
	Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
	145 150 155	
	ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat	527
35	Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	
	160 165 170 175	
	gca cac aaa gcc atc tgg cat gag tgc cct ctg ggc tgg ctg ctg cac	575
40	Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	
	180 185 190	
	aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg	623
	Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	
	195 200 205	
45		

39

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	Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly	
	210 215 220	
5	ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg	719
	Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu	
	225 230 235	
10	ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg	767
	Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu	
	240 245 250 255	
15	gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg	815
	Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met	
	260 265 270	
20	aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt	863
	Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly	
	275 280 285	
	ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att	911
	Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile	
	290 295 300	
25	cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg	959
	Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp	
	305 310 315	
30	tcc aag cgg tag ggtgcggaac caggcacgct gggttcacac ctcatgcctg	1011
	Ser Lys Arg	
	320	
	tgataaggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggtctga	1071
35	tggccaatgg catcgccat gtctggtcat cacgggctgg ttgcctgggt gaaggtgatg	1131
	cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc	1191
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	catattctat ttgtgggagc tgagatgatg gcatgcttgg gatgtgcatg gatcatggta	1311
	gtgcagcaaa ctatattcac ctagggtgtg tggtaggatc aggtgaggcc ttgcacattg	1371
45	catgatgtac tcgtcatggt gtgttggtga gaggatggat gtggatggat gtgtattctc	1431

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 ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551
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 15 <213> Haematococcus pluvialis

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 20 25 30
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 35 40 45
 Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
 50 55 60
 35 Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
 65 70 75 80
 40 Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
 85 90 95
 45 Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg

	100	105	110
5	Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val 115 120 125		
10	Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met 130 135 140		
15	Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu 145 150 155 160		
20	Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala 165 170 175		
25	His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys 180 185 190		
30	Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe 195 200 205		
35	Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe 210 215 220		
40	Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly 225 230 235 240		
45	Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val 245 250 255		
	His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys 260 265 270		
	Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly 275 280 285		

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
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Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
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Lys Arg

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<222> (1)..(1503)

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<400> 19

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 1 5 10 15

40

cat cat ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat 96
 His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
 20 25 30

45

cat aat ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt 144
 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val

	35	40	45	
5	tgt gtt aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr	192		
	50	55	60	
10	aaa aag gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys	240		
	65	70	75	80
	ggg gtt gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	288		
	85	90	95	
15	gct gtt gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile	336		
	100	105	110	
20	gat ccg aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	384		
	115	120	125	
25	gat gaa ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp	432		
	130	135	140	
30	tct ggt gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His	480		
	145	150	155	160
	aga cct tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met	528		
	165	170	175	
35	cag aaa tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile	576		
	180	185	190	
40	aag gtg att cat gag gaa tcg aaa tcc atg ttg ata tgc aat gat ggt Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly	624		
	195	200	205	
45	att act att cag gca acg gtg gtg ctc gat gca act ggc ttc tct aga Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg	672		
	210	215	220	

	tct ctt gtt cag tat gat aag cct tat aac ccc ggg tat caa gtt gct	720
	Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala	
	225 230 235 240	
5	tat ggc att ttg gct gaa gtg gaa gag cac ccc ttt gat gta aac aag	768
	Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys	
	245 250 255	
10	atg gtt ttc atg gat tgg cga gat tct cat ttg aag aac aat act gat	816
	Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp	
	260 265 270	
	ctc aag gag aga aat agt aga ata cca act ttt ctt tat gca atg cca	864
15	Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro	
	275 280 285	
	ttt tca tcc aac agg ata ttt ctt gaa gaa aca tca ctc gta gct cgt	912
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	Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu	
	305 310 315 320	
25	aac cat ttg ggg ata aaa gtg aag agc att gaa gaa gat gaa cat tgt	1008
	Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys	
	325 330 335	
30	cta ata cca atg ggt ggt cca ctt cca gta tta cct cag aga gtc gtt	1056
	Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val	
	340 345 350	
	gga atc ggt ggt aca gct ggc atg gtt cat cca tcc acc ggt tat atg	1104
35	Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met	
	355 360 365	
	gtg gca agg aca cta gct gcg gct cct gtt gtt gcc aat gcc ata att	1152
	Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile	
40	370 375 380	
	caa tac ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca	1200
	Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr	
	385 390 395 400	

45

	gct gtt tgg aaa gat ttg tgg cct ata gag agg aga cgt caa aga gag	1248
	Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu	
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	Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala	
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10	aca aga agg ttc ttt gat gca ttc ttt gac tta gaa cct cgt tat tgg	1344
	Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp	
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15	cat ggc ttc tta tgc tct cga ttg ttt cta cct gaa ctc ata gtt ttt	1392
	His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe	
	450 455 460	
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	Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile	
	465 470 475 480	
	atg aca aag gga act gtt cca tta gta aat atg atc aac aat ttg tta	1488
	Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu	
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 20 25 30

5 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45

10 Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60

15 Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80

Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
 85 90 95

20 Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
 100 105 110

25 Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
 115 120 125

30 Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
 130 135 140

35 Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His
 145 150 155 160

Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
 165 170 175

40 Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile
 180 185 190

45 Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly

	195	200	205
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10	Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala 225 230 235 240		
15	Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys 245 250 255		
20	Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp 260 265 270		
25	Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro 275 280 285		
30	Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg 290 295 300		
35	Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu 305 310 315 320		
40	Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys 325 330 335		
45	Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val 340 345 350		
	Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met 355 360 365		
	Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile 370 375 380		

5 Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr
 385 390 395 400

10 Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415

15 Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
 420 425 430

20 Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
 435 440 445

25 His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
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30 Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
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40 Gln Asp Lys Glu
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 40 <213> Potato

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<221> Intron

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<400> 21

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gttgatgtgc agctg 195

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<213> Haematococcus pluvialis

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<222> (6)..(995)

<223>

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<400> 22

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Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser

1

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10

15

45

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51

	Asp	Phe	His	Arg	Gly	Asn	Pro	Gly	Ile	Val	Pro	Trp	Phe	Ala	Ser	Phe	
				195					200					205			
	atg	tcc	agc	tac	atg	tcg	atg	tgg	cag	ttt	gcg	cgc	ctc	gca	tgg	tgg	674
5	Met	Ser	Ser	Tyr	Met	Ser	Met	Trp	Gln	Phe	Ala	Arg	Leu	Ala	Trp	Trp	
			210					215					220				
	acg	gtg	gtc	atg	cag	ctg	ctg	ggc	gcg	cca	atg	gcg	aac	ctg	ctg	gtg	722
10	Thr	Val	Val	Met	Gln	Leu	Leu	Gly	Ala	Pro	Met	Ala	Asn	Leu	Leu	Val	
			225					230					235				
	ttc	atg	gcg	gcc	gcg	ccc	atc	ctg	tcc	gcc	ttc	cgc	ttg	ttc	tac	ttt	770
	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	Ser	Ala	Phe	Arg	Leu	Phe	Tyr	Phe	
15			240				245					250				255	
	ggc	acg	tac	atg	ccc	cac	aag	cct	gag	cct	ggc	gcc	gcg	tca	ggc	tct	818
	Gly	Thr	Tyr	Met	Pro	His	Lys	Pro	Glu	Pro	Gly	Ala	Ala	Ser	Gly	Ser	
					260					265					270		
20	tca	cca	gcc	gtc	atg	aac	tgg	tgg	aag	tcg	cgc	act	agc	cag	gcg	tcc	866
	Ser	Pro	Ala	Val	Met	Asn	Trp	Trp	Lys	Ser	Arg	Thr	Ser	Gln	Ala	Ser	
				275					280					285			
	gac	ctg	gtc	agc	ttt	ctg	acc	tgc	tac	cac	ttc	gac	ctg	cac	tgg	gag	914
25	Asp	Leu	Val	Ser	Phe	Leu	Thr	Cys	Tyr	His	Phe	Asp	Leu	His	Trp	Glu	
			290					295					300				
	cac	cac	cgc	tgg	ccc	ttt	gcc	ccc	tgg	tgg	gag	ctg	ccc	aac	tgc	cgc	962
30	His	His	Arg	Trp	Pro	Phe	Ala	Pro	Trp	Trp	Glu	Leu	Pro	Asn	Cys	Arg	
			305				310					315					
	cgc	ctg	tct	ggc	cga	ggc	ctg	gtt	cct	gcc	tag	ctggacacac	tg	cagtgggc			1015
	Arg	Leu	Ser	Gly	Arg	Gly	Leu	Val	Pro	Ala							
35							320										
	cctgctgcca	gctgggcatg	caggttgtgg	caggactggg	tgaggtgaaa	agctgcaggc											1075
	gctgctgccg	gacacgctgc	atgggctacc	ctgtgtagct	gccgccacta	ggggaggggg											1135
40	ttttagctg	tcgagcttgc															1155

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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

25

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

30

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

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Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

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Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

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Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

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Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

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His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

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Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

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Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

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Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

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Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

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Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

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Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

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Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
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Ser Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu	
20 25 30	

35 gag tca gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca 144

Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro	
35 40 45	

40 cct tcc gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc 192

Pro Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser	
50 55 60	

45 tgg gcc gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc 240

Trp Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr	
65 70 75	

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	tcc ttg gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag	288
	Ser Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln	
	80 85 90 95	
5	ctg gtt agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt	336
	Leu Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe	
	100 105 110	
10	gtc ctg gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct	384
	Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala	
	115 120 125	
15	atg cat ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg	432
	Met His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu	
	130 135 140	
20	ggc aga gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg	480
	Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu	
	145 150 155	
	cac cgc aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag	528
	His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
	160 165 170 175	
25	gac cct gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc	576
	Asp Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala	
	180 185 190	
30	agc ttc atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca	624
	Ser Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala	
	195 200 205	
35	tgg tgg acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg	672
	Trp Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu	
	210 215 220	
40	ctg gtg ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc	720
	Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe	
	225 230 235	
	tac ttt ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca	768
	Tyr Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser	
	240 245 250 255	
45	ggc tct tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag	816

56

Gly Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln
 260 265 270

5 gcg tcc gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac 864
 Ala Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His
 275 280 285

10 tgg gag cac cac cgc tgg ccc ttc gcc ccc tgg tgg gag ctg ccc aac 912
 Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn
 290 295 300

tgc cgc cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac 961
 Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 305 310 315

15 tgcagtgggc cctgctgcca gctgggcatg caggttgtgg caggactggg tgaggtgaaa 1021
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Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro
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Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp
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Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser
 65 70 75 80

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Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu
 85 90 95

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Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val
 100 105 110

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Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met
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His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly
 130 135 140

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Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His
 145 150 155 160

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Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp
 165 170 175

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Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser
 180 185 190

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Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp
 195 200 205

Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu
 210 215 220

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58

Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr
 225 230 235 240

5 Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly
 245 250 255

10 Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala
 260 265 270

15 Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp
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	1 5 10 15	
5	gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac	98
	Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp	
	20 25 30	
	gtg ttg cgt aca tgg gcg acc cag tac tgc ctt ccg tca gag gag tca	146
10	Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser	
	35 40 45	
	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc	194
15	Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser	
	50 55 60	
	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gct	242
	Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala	
	65 70 75	
20	gca gtg ttc ctc cag gcc att ttt caa atc aag ctt ccg acc tcc ttg	290
	Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu	
	80 85 90 95	
25	gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt	338
	Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val	
	100 105 110	
	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg	386
30	Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu	
	115 120 125	
	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat	434
35	Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His	
	130 135 140	
	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga	482
	Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg	
	145 150 155	
40	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc	530
	Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg	
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<213> Haematococcus pluvialis

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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

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Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

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Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

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Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

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Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

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Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly

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	Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val		
5	145	150	155 160
	Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys		
10	165	170	175
	His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp		
	180	185	190
15	Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met		
	195	200	205
20	Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr		
	210	215	220
	Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe		
25	225	230	235 240
	Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly		
30	245	250	255
	Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser		
	260	265	270
35	Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp		
	275	280	285
40	Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His		
	290	295	300
	His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg		
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Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser Glu
 325 330 335

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Glu Asp Leu Asn Ser
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<211> 777

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35

agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga 180

ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240

40

ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

tatatatctc tttcttctta tttcccaaata taacagacaa aagtagaata ttggctttta 420

45

64

acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
5 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt 660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
10 tctttcttct cattatatct cttgtcctct ccaccaaate tttcaacaa aaagctt 777

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40 <211> 24
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 10 aaatttggtg atgtgcaggt atcacggat cc 212

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 agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
 Met Ser Met Arg Ala Gly His Met Thr Ala Thr
 40 1 5 10
 atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221
 Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
 15 20 25
 45

70

	aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa	269
	Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln	
	30 35 40	
5	gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg	317
	Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu	
	45 50 55	
10	ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc	365
	Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser	
	60 65 70 75	
15	cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt	413
	Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser	
	80 85 90	
20	aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt	461
	Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu	
	95 100 105	
25	gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc	509
	Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile	
	110 115 120	
30	ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa	557
	Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu	
	125 130 135	
35	ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat	605
	Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp	
	140 145 150 155	
40	act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc	653
	Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala	
	160 165 170	
45	tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg	701
	Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg	
	175 180 185	
50	tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749
	Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
	190 195 200	
55	act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797

	Thr	Glu	Ala	Pro	Asn	Gly	Leu	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	
	205						210					215					
5	aca	att	cca	tgc	agg	ctt	gct	act	gtc	gct	tct	gga	gca	gct	tct	gga	845
	Thr	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	
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10	aaa	ctt	ttg	cag	tat	gaa	ctt	ggc	ggc	ccc	cgt	gtt	tgc	gtt	caa	aca	893
	Lys	Leu	Leu	Gln	Tyr	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	
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15	gct	tat	ggc	ata	gag	gtt	gag	gtt	gaa	agc	ata	ccc	tat	gat	cca	agc	941
	Ala	Tyr	Gly	Ile	Glu	Val	Glu	Val	Glu	Ser	Ile	Pro	Tyr	Asp	Pro	Ser	
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20	cta	atg	gtt	ttc	atg	gat	tat	aga	gac	tac	acc	aaa	cat	aaa	tct	caa	989
	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	His	Lys	Ser	Gln	
			270					275					280				
25	tca	cta	gaa	gca	caa	tat	cca	aca	ttt	ttg	tat	gtc	atg	cca	atg	tct	1037
	Ser	Leu	Glu	Ala	Gln	Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	
		285					290					295					
30	cca	act	aaa	gta	ttc	ttt	gag	gaa	act	tgt	ttg	gct	tca	aaa	gag	gcc	1085
	Pro	Thr	Lys	Val	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Glu	Ala	
		300				305					310				315		
35	atg	cct	ttt	gag	tta	ttg	aag	aca	aaa	ctc	atg	tca	aga	tta	aag	act	1133
	Met	Pro	Phe	Glu	Leu	Leu	Lys	Thr	Lys	Leu	Met	Ser	Arg	Leu	Lys	Thr	
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40	atg	ggg	atc	cga	ata	acc	aaa	act	tat	gaa	gag	gaa	tgg	tca	tat	att	1181
	Met	Gly	Ile	Arg	Ile	Thr	Lys	Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	
				335					340					345			
45	cca	gta	ggc	gga	tcc	tta	cca	aat	acc	gag	caa	aag	aac	ctt	gca	ttt	1229
	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu	Gln	Lys	Asn	Leu	Ala	Phe	
			350				355						360				
50	ggc	gct	gct	gct	agc	atg	gtg	cat	cca	gcc	aca	gga	tat	tcg	gtt	gta	1277
	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	
		365					370					375					
55	aga	tca	ctg	tca	gaa	gct	cct	aat	tat	gca	gca	gta	att	gca	aag	att	1325
	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Asn	Tyr	Ala	Ala	Val	Ile	Ala	Lys	Ile	

	380	385	390	395	
	tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca				1373
	Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr				
5	400		405	410	
	acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg				1421
	Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg				
10	415		420	425	
	aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag				1469
	Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln				
	430		435	440	
15	atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg				1517
	Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu				
	445		450	455	
	ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act				1565
20	Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr				
	460		465	470	475
	gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc				1613
	Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser				
25	480		485	490	
	ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga				1661
	Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly				
30	495		500	505	
	aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag				1711
	Thr Met Leu Lys Ala Tyr Leu Thr Ile				
	510		515		
35	tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct				1771
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<213> Tagetes erecta

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Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
 20 25 30

15

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
 35 40 45

20

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60

25

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80

30

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110

35

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
 115 120 125

40

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
 130 135 140

45

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
 145 150 155 160

Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
 165 170 175

5 Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
 180 185 190

10 Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
 195 200 205

15 Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
 210 215 220

20 Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
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Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255

25 Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
 260 265 270

30 Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285

35 Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300

40 Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
 305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
 325 330 335

45

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350

5 Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
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10 Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380

15 Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn
 385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415

20 Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430

25 Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445

30 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460

35 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
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45 Tyr Leu Thr Ile

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gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180
30 ggccggtttt acatgcccta gggtttatgac tagcatcaga tacacgaagc aaattaagtg 240
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35 gaaagccggt ggatcggagc tgctttttgt tcaaagcaa cagaataagt ccatggatgc 360
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gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240

25 caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

gaaagccggt ggatcggagc tgctttttgt tcaaagcaa cagaataagt ccatggatgc 360

30 acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420

ctgtatactg gatttggttg gaccc 446

35 <210> 42

<211> 393

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5 <222> (1)..(393)

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gactttcttc cgcttgccca catggatgtg gtgggggttt cttggatctt cgttatcatc 120

15

aactgacttg ataatatattg cgttttacat gtttatcata gcaccgcata gcctgagaat 180

gggtctggtt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240

20

cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata 300

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25

<210> 43

<211> 397

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<212> DNA

<213> Tagetes erecta

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<220>

<221> Antisense fragment

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40	acctcaaaaa caacgacaag tttccgaaca gtcgcgaaga tcaagggtat aatcgtcttt	1380
	ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt	1440
	taaaacgtag ctgctgttta agtaaattccc agtccttcag tttgtgcttt tgtgtgtttt	1500
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5 <211> 734

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10 <213> Artificial sequence

<220>

15 <221> variation

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30	gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc	240
	caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat	300
	gatattttaga tagattagct atcacctgtg ctgtgggtgtg cagctcccaa gggctttacc	360
35	gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg	420
	tgagaatggt gagaaagagg ttgacaaat cgggtgtttga atgaggttaa atggagtta	480
40	attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata	540
	tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct	600
45	tggtgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta	660

ttgaatgcaa agcaaagcaa aggttggttg ttgttggtgt tgagagacac tccaatccaa 720
 acagatacaa ggcg 734

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attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaaa acatacaacg 120

30 tggcgtttaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180

aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggtgt ttgttggtgt 240

35 tgttgagaga cactccaatc caaacagata caaggcgtga 280

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40 <211> 358

<212> DNA

<213> Tagetes erecta

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5 <221> Sense promoter

<222> (1)..(358)

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tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180

20 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240

aagatggctt ggctgctaâ caactcaact caactcatat cctatccatt caaattcaat 300

tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtg tttgttgtg ttgtcgac 358

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<211> 361

30 <212> DNA

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40 <222> (1)..(361)

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taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgagggt 120
aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa 180
10 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300
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15 c 361

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20 <211> 28
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25 <213> Artificial sequence

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30 <221> Primer
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35 <223>

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40 gagctcactc actgatttcc attgcttg 28
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<211> 37

<212> DNA

5 <213> Artificial sequence

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20 cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

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<210> 51

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<211> 34

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45 atcaacggac atcgacttaa cggcgtttgt aaac

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5 <210> 52
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taagcttttt gttgaagaga tttgg

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gaaaatacct catcagcatt acc 23

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30 <210> 55

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<210> 57

35 <211> 29

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<223>

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gtcgacaacc aaatccagta tacagttac

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aggatccaac caaatccagt atacagttac

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gaattcgcac gaggcaaagc aaaggttg

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15 <210> 60

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gtcgacagaa aatacttcat cagcattac

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<211> 29

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ggatccagaa aatacttcat cagcattac

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<210> 63

<211> 27

<212> DNA

5 <213> Artificial sequence

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10 <221> Primer

<222> (1)..(27)

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<400> 63

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<210> 64

25 <211> 23

<212> DNA

<213> Artificial sequence

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35 <221> Primer

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<400> 64

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 <220>
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 <400> 65
 ctaacaatca atgagtatga gagc

24

25

 <210> 66
 <211> 26

30

 <212> DNA
 <213> Artificial sequence

35

 <220>
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40 <222> (1)..(26)
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<400> 66
agagcaaggc cagcaggacc acaacc

26

5 <210> 67

<211> 26

<212> DNA

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<213> Artificial sequence

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<221> Primer

<222> (1)..(26)

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25 <400> 67

ccttgggagc ttttgggata ggctag

26

<210> 68

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<211> 26

<212> DNA

35 <213> Artificial sequence

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<221> Primer

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tcacgccttg tatctgtttg gattgg

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<210> 69

10 <211> 15

<212> DNA

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<212> DNA

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aagcttaccg atagtaaaat cgttagtt

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<212> DNA

<213> Artificial sequence

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<210> 72

<211> 28

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<213> Artificial sequence

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<400> 72

gtcgacaaca acaacaaaaca accttttgc

28

<210> 73

5

<211> 28

<212> DNA

10 <213> Artificial sequence

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15

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25

ggatccaaca acaacaaaaca accttttgc

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45

<400> 74

gtcgaactttt tgttgaagag atttggtg

28

5

<210> 75

<211> 28

10

<212> DNA

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<221> Primer

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<400> 75

ctcgagactc actgatttcc attgcttg

28

30

<210> 76

<211> 22

35

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22

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<210> 77

<211> 23

15

<212> DNA

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<223>

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<400> 77

aagcttatta tttccaaatt ccg

23

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<210> 78

<211> 50

<212> DNA

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<220>

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5 <222> (1)..(50)

<223>

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<400> 78

aagctttgca attcatacag aagtgagaaa aatgcagcta gcagcgacag

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15 <210> 79

<211> 1062

<212> DNA

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<213> Haematococcus pluvialis

25 <220>

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<222> (32)..(1021)

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<223>

35 <400> 79

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52

Met Gln Leu Ala Ala Thr Val

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40 atg ttg gag cag ctt acc gga agc gct gag gca ctc aag gag aag gag

100

Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys Glu Lys Glu

10

15

20

aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg gcg acc cag

148

45 Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp Ala Thr Gln

	25		30		35	
	tac tgc ctt ccg tca gag gag tca gac gcg gcc cgc ccg gga ctg aag					196
	Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys					
5	40		45		50	55
	aat gcc tac aag cca cca cct tcc gac aca aag ggc atc aca atg gcg					244
	Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile Thr Met Ala					
		60		65		70
10						
	cta gct gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac gcc att ttt					292
	Leu Ala Val Ile Gly Ser Trp Ala Ala Val Phe Leu His Ala Ile Phe					
		75		80		85
	caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg ctg ccc gtg					340
15	Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp Leu Pro Val					
		90		95		100
	tca gat gcc aca gct cag ctg gtt agc ggc agc agc agc ctg ctg cac					388
20	Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Ser Ser Ser Leu Leu His					
		105		110		115
	atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca ggc ctt ttt					436
	Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe					
25	120		125		130	135
	atc acc acg cat gat gct atg cat ggc acc atc gcc atg aga aac agg					484
	Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met Arg Asn Arg					
		140		145		150
30						
	cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg tac gcc tgg					532
	Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp					
		155		160		165
	ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac cac aac cac					580
35	Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His His Asn His					
		170		175		180
	act ggc gag gtg ggc aag gac cct gac ttc cac agg gga aac cct ggc					628
40	Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly Asn Pro Gly					
		185		190		195
	att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg tgc atg tgg					676
	Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Met Trp					
45	200		205		210	215

cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag ctg ctg ggt 724
 Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln Leu Leu Gly
 220 225 230

5 gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg ccc atc ctg 772
 Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu
 235 240 245

10 tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc cac aag cct 820
 Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro His Lys Pro
 250 255 260

15 gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg aac tgg tgg 868
 Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met Asn Trp Trp
 265 270 275

20 aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt ctg acc tgc 916
 Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe Leu Thr Cys
 280 285 290 295

25 tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc ttt gcc ccc 964
 Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro
 300 305 310

tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga ggt ctg gtt 1012
 Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 315 320 325

30 cct gcc tag ctggacacac tgcagtgggc cctgctgccca gctgggcatg c 1062
 Pro Ala

35 <210> 80
 <211> 329
 <212> PRT

40 <213> Haematococcus pluvialis

45 <400> 80

Met Gln, Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
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 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

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 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

15
 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

20
 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

25
 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

30
 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

35
 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

40
 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

45
 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

50
 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

104

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

5 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

10 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

15 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

20 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

25 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

30 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

35 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
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40 <210> 81
 <211> 831

<212> DNA

<213> Haematococcus pluvialis

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<400> 81

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Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala

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10

15

tat aaa cct cca gca tct gac gcc aag ggc atc act atg gcg ctg acc 96

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr

20

25

30

25

atc att ggc acc tgg acc gca gtg ttt tta cac gca ata ttc caa atc 144

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile

35

40

45

30

agg cta ccg aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa 192

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu

50

55

60

gcc aca gcc cag ctg ttg ggc gga agc agc agc cta ttg cac atc gcc 240

35

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala

65

70

75

80

gca gtc ttc att gta ctt gag ttt ctg tac act ggt cta ttc atc acc 288

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr

40

85

90

95

acg cat gat gca atg cat ggc acc ata gct ttg agg aac agg cag ctc 336

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu

100

105

110

45

106

	aat gat ctc ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac	384
	Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp	
	115 120 125	
5	tac agc atg cac tgg gag cac cac aac cat act ggc gaa gtg ggg aaa	432
	Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
	130 135 140	
10	gac cct gac ttc cac aaa gga aat cct ggc ctt gtc ccc tgg ttc gcc	480
	Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala	
	145 150 155 160	
15	agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg gca	528
	Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala	
	165 170 175	
20	tgg tgg gca gtg gtg atg caa acg ttg ggg gcc ccc atg gcg aat ctc	576
	Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu	
	180 185 190	
25	cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc ttc	624
	Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe	
	195 200 205	
30	ggc tct cag gtc atg tct tgg ttc agg gcc aag aca agt gag gca tct	720
	Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser	
	225 230 235 240	
35	gat gtg atg agc ttc ctg aca tgc tac cac ttt gac ctg ttt gcc ccc	768
	Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro	
	245 250 255	
40	tgg tgg cag ctg ccc cac tgc cgc cgc ctg tct ggg cgt ggc ctg gtg	816
	Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val	
	260 265 270	
45	cct gcc ttg gca tga	831
	Pro Ala Leu Ala	
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<210> 82

<211> 276

5 <212> PRT

<213> Haematococcus pluvialis

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<400> 82

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala

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Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr

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25

30

20

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile

35

40

45

25

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu

50

55

60

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala

30

65

70

75

80

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr

85

90

95

35

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu

100

105

110

40

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp

115

120

125

45

Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys

130

135

140

5 Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala
145 150 155 160

10 Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala
165 170 175

15 Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu
180 185 190

20 Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe
195 200 205

25 Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala
210 215 220

30 Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser
225 230 235 240

35 Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
245 250 255

40 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
260 265 270

45 Pro Ala Leu Ala
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<210> 83

<211> 729

<212> DNA

<213> Paracoccus sp. MBIC1143

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<222> (1)..(729)

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20 atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat	96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	
20 25 30	

25 gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	

30 aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	

35 gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	

40 cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	

45 gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	

110

	115	120	125	
	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc			432
	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro			
5	130	135	140	
	gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac			480
	Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr			
	145	150	155	160
10				
	gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc			528
	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe			
	165	170	175	
15	gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg			576
	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro			
	180	185	190	
	gac cgc cac aat gcg ccg tcg tcg ccg atc agc gac ccc gtg tcg ctg			624
20	Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu			
	195	200	205	
	ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac			672
	Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His			
25	210	215	220	
	ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac			720
	Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp			
	225	230	235	240
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	acc gca tga			729
	Thr Ala			
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<400> 84

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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

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 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

15
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

20
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

25
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

30
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

35
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

40
 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

45
 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

5 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

10 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

15 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

Thr Ala

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<210> 85

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<213> Brevundimonas aurantiaca

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45 1 5 10 15

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5	cat gtc tac ggc gtc tat ttt cac cga tgg ggg ccg ttg acc ctg gtg His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val 35 40 45	144
10	atc gcc ccg gcg atc gtg gcg gtc cag acc tgg ttg tcg gtc ggc ctt Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu 50 55 60	192
15	ttc atc gtc gcc cat gac gcc atg tac ggc tcc ctg gcg ccg gga cgg Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg 65 70 75 80	240
20	ccg cgg ctg aac gcc gca gtc ggc cgg ctg acc ctg ggg ctc tat gcg Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala 85 90 95	288
25	ggc ttc cgc ttc gat cgg ctg aag acg gcg cac cac gcc cac cac gcc Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala 100 105 110	336
30	gcg ccc ggc acg gcc gac gac ccg gat ttt cac gcc ccg gcg ccc cgc Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg 115 120 125	384
35	gcc ttc ctt ccc tgg ttc ctg aac ttc ttt cgc acc tat ttc ggc tgg Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp 130 135 140	432
40	cgc gag atg gcg gtc ctg acc gcc ctg gtc ctg atc gcc ctc ttc ggc Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly 145 150 155 160	480
45	ctg ggg gcg cgg ccg gcc aat ctc ctg acc ttc tgg gcc gcg ccg gcc Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala 165 170 175	528
	ctg ctt tca gcg ctt cag ctc ttc acc ttc ggc acc tgg ctg ccg cac Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His 180 185 190	576

114

	cgc cac acc gac cag ccg ttc gcc gac gcg cac cac gcc cgc agc agc	624
	Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser	
	195 200 205	
5	ggc tac ggc ccc gtg ctt tcc ctg ctc acc tgt ttc cac ttc ggc cgc	672
	Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg	
	210 215 220	
10	cac cac gaa cac cat ctg agc ccc tgg cgg ccc tgg tgg cgt ctg tgg	720
	His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp	
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40	His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val	
	35 40 45	
45	Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu	
	50 55 60	

115

Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg
 65 70 75 80

5 Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala
 85 90 95

10 Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala
 100 105 110

15 Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg
 115 120 125

Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp
 130 135 140

20 Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly
 145 150 155 160

25 Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala
 165 170 175

30 Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
 180 185 190

35 Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

40 Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

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 225 230 235 240

Arg Gly Glu Ser

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 1 5 10 15
 30 ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96
 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30
 35 ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144
 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45
 gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat 192
 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60
 40 ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa 240
 Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80
 45 aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa 288

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<400> 88

Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
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Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30

15

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45

20

Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
 85 90 95

30

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
 100 105 110

35

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
 115 120 125

40

Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
 130 135 140

Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu

119

145 150 155 160
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
 5 165 170 175
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 10 180 185 190
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 15 195 200 205
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 210 215 220
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	1			5						10					15		
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	Leu	Ser	Ala	Lys	Glu	Asp	Thr	Val	Trp	Gly	Leu	Val	Ile	Val	Ile	Val	
				20					25					30			
10	att	att	agt	ctt	tgg	gta	gct	agt	ttg	gct	ttt	tta	cta	gct	att	aat	144
	Ile	Ile	Ser	Leu	Trp	Val	Ala	Ser	Leu	Ala	Phe	Leu	Leu	Ala	Ile	Asn	
			35					40					45				
15	tat	gcc	aaa	gtc	cca	att	tgg	ttg	ata	cct	att	gca	ata	gtt	tgg	caa	192
	Tyr	Ala	Lys	Val	Pro	Ile	Trp	Leu	Ile	Pro	Ile	Ala	Ile	Val	Trp	Gln	
		50					55					60					
20	atg	ttc	ctt	tat	aca	ggg	cta	ttt	att	act	gca	cat	gat	gct	atg	cat	240
	Met	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ala	His	Asp	Ala	Met	His	
	65					70				75				80			
25	ggg	tca	gtt	tat	cgt	aaa	aat	ccc	aaa	att	aat	aat	ttt	atc	ggt	tca	288
	Gly	Ser	Val	Tyr	Arg	Lys	Asn	Pro	Lys	Ile	Asn	Asn	Phe	Ile	Gly	Ser	
					85				90					95			
30	cta	gct	gta	gcg	ctt	tac	gct	gtg	ttt	cca	tat	caa	cag	atg	tta	aag	336
	Leu	Ala	Val	Ala	Leu	Tyr	Ala	Val	Phe	Pro	Tyr	Gln	Gln	Met	Leu	Lys	
				100					105					110			
35	aat	cat	tgc	tta	cat	cat	cgt	cat	cct	gct	agc	gaa	gtt	gac	cca	gat	384
	Asn	His	Cys	Leu	His	His	Arg	His	Pro	Ala	Ser	Glu	Val	Asp	Pro	Asp	
			115					120					125				
40	ttt	cat	gat	ggg	aag	aga	aca	aac	gct	att	ttc	tgg	tat	ctc	cat	ttc	432
	Phe	His	Asp	Gly	Lys	Arg	Thr	Asn	Ala	Ile	Phe	Trp	Tyr	Leu	His	Phe	
		130					135					140					
45	atg	ata	gaa	tac	tcc	agt	tgg	caa	cag	tta	ata	gta	cta	act	atc	cta	480
	Met	Ile	Glu	Tyr	Ser	Ser	Trp	Gln	Gln	Leu	Ile	Val	Leu	Thr	Ile	Leu	
	145					150				155					160		
50	ttt	aat	tta	gct	aaa	tac	gtt	ttg	cac	atc	cat	caa	ata	aat	ctc	atc	528
	Phe	Asn	Leu	Ala	Lys	Tyr	Val	Leu	His	Ile	His	Gln	Ile	Asn	Leu	Ile	
					165				170					175			
55	tta	ttt	tgg	agt	att	cct	cca	att	tta	agt	tcc	att	caa	ctg	ttt	tat	576
	Leu	Phe	Trp	Ser	Ile	Pro	Pro	Ile	Leu	Ser	Ser	Ile	Gln	Leu	Phe	Tyr	

121

	180	185	190	
	ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat			624
	Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr			
5	195	200	205	
	ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
	Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
	210	215	220	
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	gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat			720
	Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
	225	230	235	240
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	gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
	Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
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	aat tca gta acc aat tcg taa			789
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	<211> 262			
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	Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val			
	20	25	30	
45				
	Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn			
	35	40	45	

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60
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Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
 65 70 75 80

10

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

15

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

20

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

25

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

30

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

35

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

40

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

45

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

123

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

5 Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

10 Asn Ser Val Thr Asn Ser
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<210> 91

15 <211> 762

<212> DNA

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25 <221> CDS

<222> (1) .. (762)

30 <223>

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 1 5 10 15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
 40 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 45 35 40 45

	atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa	192
	Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln	
	50 55 60	
5	aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat	240
	Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His	
	65 70 75 80	
10	ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca	288
	Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr	
	85 90 95	
15	ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa	336
	Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys	
	100 105 110	
20	aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat	384
	Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp	
	115 120 125	
25	ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt	432
	Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe	
	130 135 140	
30	atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att	480
	Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile	
	145 150 155 160	
35	tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act	528
	Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr	
	165 170 175	
40	tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat	576
	Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr	
	180 185 190	
45	ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag	624
	Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln	
	195 200 205	
50	cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc	672
	Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile	
	210 215 220	

125

acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat 720
 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

5 att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag 762
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 245 250

10 <210> 92
 <211> 253
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15 <213> Nostoc punctiforme ATCC 29133

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25 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
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30 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 35 40 45

35 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

40 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

45

126

	Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys	
	100	105 110
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10	Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe	
	130	135 140
15	Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile	
	145	150 155 160
20	Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr	
	165	170 175
25	Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr	
	180	185 190
30	Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln	
	195	200 205
35	Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile	
	210	215 220
40	Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His	
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<213> *Deinococcus radiodurans* R1

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<222> (1)..(1536)

<223>

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<400> 93

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5

10

15

gtg act gct gcc tac gcc gcc cgg gcg ggc ctg aaa gtc ggc gtg ttc 96

Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe

20

25

30

25

gag cgg cgg cac ctc gtc ggc ggg gcg gtc agc acc gag gag gtc gtg 144

Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val

35

40

45

30

ccc ggt tac cgc ttc gac tac ggc ggc agc gcc cac atc ctg att cgg 192

Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg

50

55

60

atg acg ccc atc gtg cgc gaa ctc gaa ctc acg cgg cac ggg ctg cat 240

35

Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His

65

70

75

80

tac ctc gaa gtg gac cct atg ttt cac gct tcc gac ggt gaa acg ccc 288

Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro

40

85

90

95

tgg ttc att cac cgc gac gcc ggg cgg acc atc cgc gaa ctg gac gaa 336

Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu

100

105

110

45

	aag ttt ccc ggg cag ggc gac gcc tac ggg cgc ttt ctc gac gat tgg	384
	Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp	
	115 120 125	
5	aca ccc ttc gcg cgc gcc gtg gcc gac ctg ttc aac tcg gcg ccg ggg	432
	Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly	
	130 135 140	
10	ccg ctc gac ctg ggc aaa atg gtg atg cgc agc ggc cag ggc aag gac	480
	Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp	
	145 150 155 160	
15	tgg aac gag cag ctc ccg cgc atc ctg cgg ccc tac ggc gac gtg gcg	528
	Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala	
	165 170 175	
20	cgc gag tac ttc agc gag gag cgc gtg cgg gct ccc ctg acc tgg atg	576
	Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met	
	180 185 190	
	gcg gcc cag agc ggc ccc cca ccc tcg gac ccg ctg agc gcg ccc ttt	624
	Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe	
	195 200 205	
25	ttg ctg tgg cac ccg ctc tac cac gaa ggc ggc gtg gcg cgg ccc aaa	672
	Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys	
	210 215 220	
30	ggc ggc agc ggc ggc ctg acc aaa gcc ctg cgc cgg gcc acc gag gcc	720
	Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala	
	225 230 235 240	
35	gaa ggc ggc gag gtc ttc acc gac gcg ccg gtc aag gaa att ctg gtc	768
	Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val	
	245 250 255	
40	aag gac ggc aag gcg cag ggc atc cgg ctg gaa agc ggc gag acg tac	816
	Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr	
	260 265 270	
	acc gcc cgc gcc gtc gtg tcg ggc gtc cac atc ctg acc act gcg aat	864
	Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn	
	275 280 285	
45	gcc ctg ccc gcc gaa tat gtc cct agc gcc gcc agg aat gtg cgc gtg	912

129

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	Gly	Asn	Gly	Phe	Gly	Met	Ile	Leu	Arg	Leu	Ala	Leu	Ser	Glu	Lys	Val	
	305				310					315						320	
10	aaa	tac	cgt	cac	cac	acc	gag	ccc	gac	tca	cgc	atc	ggc	ctg	gga	ttg	1008
	Lys	Tyr	Arg	His	His	Thr	Glu	Pro	Asp	Ser	Arg	Ile	Gly	Leu	Gly	Leu	
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15	ctg	atc	aaa	aac	gag	cgg	caa	atc	atg	cag	ggc	tac	ggc	gaa	tac	ctc	1056
	Leu	Ile	Lys	Asn	Glu	Arg	Gln	Ile	Met	Gln	Gly	Tyr	Gly	Glu	Tyr	Leu	
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	Ala	Gly	Gln	Pro	Thr	Thr	Asp	Pro	Pro	Leu	Val	Ala	Met	Ser	Phe	Ser	
		355					360					365					
25	gcg	gtg	gac	gac	tcg	ctc	gcc	cca	ccg	aac	ggc	gac	gtg	ttg	tgg	ctg	1152
	Ala	Val	Asp	Asp	Ser	Leu	Ala	Pro	Pro	Asn	Gly	Asp	Val	Leu	Trp	Leu	
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	Trp	Ala	Gln	Tyr	Tyr	Pro	Phe	Glu	Leu	Ala	Thr	Gly	Ser	Trp	Glu	Thr	
	385				390					395				400			
35	cgc	acc	gcc	gaa	gcg	cgg	gag	aac	atc	ctg	cgg	gcc	ttt	gag	cac	tac	1248
	Arg	Thr	Ala	Glu	Ala	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Phe	Glu	His	Tyr	
			405				410						415				
40	gcg	ccg	ggc	acc	cgc	gac	acg	att	gtg	ggc	gaa	ctc	gtg	cag	acg	ccg	1296
	Ala	Pro	Gly	Thr	Arg	Asp	Thr	Ile	Val	Gly	Glu	Leu	Val	Gln	Thr	Pro	
			420				425					430					
45	cag	tgg	ctg	gaa	acc	aac	ctc	ggc	ctg	cac	cgg	ggc	aac	gtg	atg	cac	1344
	Gln	Trp	Leu	Glu	Thr	Asn	Leu	Gly	Leu	His	Arg	Gly	Asn	Val	Met	His	
		435					440					445					
50	ctg	gaa	atg	tcc	ttc	gac	cag	atg	ttc	tcc	ttc	cgc	ccc	tgg	ctg	aaa	1392
	Leu	Glu	Met	Ser	Phe	Asp	Gln	Met	Phe	Ser	Phe	Arg	Pro	Trp	Leu	Lys	
		450					455					460					
55	gcg	agc	cag	tac	cgc	tgg	ccg	ggc	gtg	cag	ggg	ctg	tac	ctc	acc	ggc	1440
	Ala	Ser	Gln	Tyr	Arg	Trp	Pro	Gly	Val	Gln	Gly	Leu	Tyr	Leu	Thr	Gly	

465 470 475 480
 gcc agc acc cac ccc ggc gga ggc atc atg ggc gcc tcg gga cgc aac 1488
 Ala Ser Thr His Pro Gly Gly Gly Ile Met Gly Ala Ser Gly Arg Asn
 5 485 490 495
 gcg gcg cgg gtc atc gtg aag gac ctg acg cgg agg cgc tgg aaa tga 1536
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 35 40 45
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 Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg
 50 55 60
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 Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His
 65 70 75 80
 Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro
 45 85 90 95

Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu
 100 105 110
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Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp
 115 120 125

10 Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly
 130 135 140

15 Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp
 145 150 155 160

20 Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala
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Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met
 180 185 190
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Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe
 195 200 205

30 Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys
 210 215 220

35 Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala
 225 230 235 240

Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val
 245 250 255
 40

Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr
 260 265 270
 45

Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn
 275 280 285

5

Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val
 290 295 300

10

Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val
 305 310 315 320

15

Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu
 325 330 335

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Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu
 340 345 350

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Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser
 355 360 365

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Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu
 370 375 380

35

Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr
 385 390 395 400

40

Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr
 405 410 415

45

Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro
 420 425 430

Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His
 435 440 445

133

Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys
 450 455 460

5 Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly
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aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc 96
 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
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134

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	Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
	35 40 45	
5	aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
	Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
	50 55 60	
10	tct tta gat gtt aac atc tca tgg gtt gat cct aat tcg aat cgg gct	240
	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
	65 70 75 80	
15	caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
	85 90 95	
20	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
	100 105 110	
25	tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
	115 120 125	
30	ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
	130 135 140	
35	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
	145 150 155 160	
40	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser	
	165 170 175	
45	tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
	180 185 190	
50	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624
	Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys	
	195 200 205	
55	ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat ttt	672

135

	Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe	
	210						215					220					
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5	Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly	
	225					230					235					240	
	gtt	tta	gta	gaa	gtt	gat	aat	cat	cca	ttt	gat	ttg	gat	aaa	atg	gtg	768
10	Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val	
					245					250					255		
	ctt	atg	gat	tgg	agg	gat	tct	cat	ttg	ggg	aat	gag	cca	tat	tta	agg	816
	Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg	
				260					265					270			
15	gtg	aat	aat	gct	aaa	gaa	cca	aca	ttc	ttg	tat	gca	atg	cca	ttt	gat	864
	Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp	
		275						280					285				
20	aga	gat	ttg	gtt	ttc	ttg	gaa	gag	act	tct	ttg	gtg	agt	cgt	cct	gtt	912
	Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val	
		290					295					300					
	tta	tcg	tat	atg	gaa	gta	aaa	aga	agg	atg	gtg	gca	aga	tta	agg	cat	960
25	Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His	
	305					310					315				320		
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30	Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile	
				325					330					335			
	cct	atg	gga	gga	cca	ctt	ccg	cgg	att	cct	caa	aat	gtt	atg	gct	att	1056
	Pro	Met	Gly	Gly	Pro	Leu	Pro	Arg	Ile	Pro	Gln	Asn	Val	Met	Ala	Ile	
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35	ggg	ggg	aat	tca	ggg	ata	gtt	cat	cca	tca	aca	ggg	tac	atg	gtg	gct	1104
	Gly	Gly	Asn	Ser	Gly	Ile	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	
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40	agg	agc	atg	gct	tta	gca	cca	gta	cta	gct	gaa	gcc	atc	gtc	gag	ggg	1152
	Arg	Ser	Met	Ala	Leu	Ala	Pro	Val	Leu	Ala	Glu	Ala	Ile	Val	Glu	Gly	
		370					375					380					
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45	Leu	Gly	Ser	Thr	Arg	Met	Ile	Arg	Gly	Ser	Gln	Leu	Tyr	His	Arg	Val	

136

	385	390	395	400	
	tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat				1248
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5		405	410	415	
	tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg				1296
	Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg				
		420	425	430	
10					
	aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg				1344
	Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly				
		435	440	445	
15					
	ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg				1392
	Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu				
		450	455	460	
	tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca				1440
20	Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr				
		465	470	475	480
	aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag				1488
	Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu				
25		485	490	495	
	agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat				1544
	Ser Leu				
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	tttcatatatt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact				1604
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15 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
 35 40 45

20 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
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25 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
 65 70 75 80

30 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
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35 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
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40 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
 115 120 125

45 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
 130 135 140

50 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
 145 150 155 160

55 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser

138

165

170

175

5 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val
180 185 190

10 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys
195 200 205

15 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe
210 215 220

Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly
225 230 235 240

20 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val
245 250 255

25 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg
260 265 270

30 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
275 280 285

Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
290 295 300

35 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
305 310 315 320

40 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile
325 330 335

45 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
340 345 350

Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
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 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
 370 375 380
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 385 390 395 400
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 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Gys Val Arg Glu Cys Tyr
 405 410 415
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 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
 420 425 430
 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
 435 440 445
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 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
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 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
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 Thr Ser Arg Thr Phe Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys
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30 cct act tcg aca acc tca cat gtt tct cca atc tct cct ttt tct ctt 148
 Pro Thr Ser Thr Thr Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu
 30 35 40

35 aat cta ggc cca att ttg agg tct aga aga aaa ccc agt ttc act gtt 196
 Asn Leu Gly Pro Ile Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val
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60 tgc ttt gtt ctc gag gat gag aag ctg aaa cct caa ttt gac gat gag 244
 Cys Phe Val Leu Glu Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu
 60 65 70 75

40 gct gag gat ttt gaa aag aag att gag gaa cag atc tta gct act cgc 292
 Ala Glu Asp Phe Glu Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg
 80 85 90

45 ttg gcg gag aaa ctg gct agg aag aaa tcg gag agg ttt act tat ctt 340
 Leu Ala Glu Lys Leu Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu

	95	100	105	
	gtg gct gct ata atg tct agt ttt ggg att act tct atg gct gtt atg			388
	Val Ala Ala Ile Met Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met			
5	110	115	120	
	gct gtt tat tac aga ttt tcg tgg caa atg gag gga gga gaa gtt cct			436
	Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro			
	125	130	135	
10				
	gta acc gaa atg ttg ggt aca ttt gct ctg tct gtt ggt gct gct gta			484
	Val Thr Glu Met Leu Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val			
	140	145	150	155
15				
	gga atg gag ttt tgg gcg aga tgg gca cac aaa gca ctg tgg cat gct			532
	Gly Met Glu Phe Trp Ala Arg Trp Ala His Lys Ala Leu Trp His Ala			
		160	165	170
	tca cta tgg cac atg cat gag tca cac cac aaa cca aga gaa gga cct			580
20	Ser Leu Trp His Met His Glu Ser His His Lys Pro Arg Glu Gly Pro			
		175	180	185
	ttt gag ctg aac gac gtt ttc gcc ata aca aac gct gtt cca gca ata			628
	Phe Glu Leu Asn Asp Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile			
25	190	195	200	
	gcc ctg ctg aac tat ggt ttc ttc cat aaa ggc ctg att gcc gga cta			676
	Ala Leu Leu Asn Tyr Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu			
	205	210	215	
30				
	tgc ttc ggt gct ggg cta ggg atc aca gta ttt gga atg gca tac atg			724
	Cys Phe Gly Ala Gly Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met			
	220	225	230	235
35				
	ttt gtt cac gat ggt ttg gtt cac aag aga ttc cca gtt gga cct gta			772
	Phe Val His Asp Gly Leu Val His Lys Arg Phe Pro Val Gly Pro Val			
		240	245	250
	gcc aat gta cct tat ctt agg aag gtg gct gct gct cat tcg ctt cat			820
40	Ala Asn Val Pro Tyr Leu Arg Lys Val Ala Ala Ala His Ser Leu His			
		255	260	265
	cac tca gag aag ttc aat ggt gtc cca tat ggc ttg ttc ttc gga cct			868
	His Ser Glu Lys Phe Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro			
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aag gaa ctg gaa gaa gta gga ggg acg gaa gag ttg gaa aag gaa gtg 916
 Lys Glu Leu Glu Glu Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val
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5 ata cga agg acg aga ctt tcg aaa gga tca tgaacgattg ttcataaaca 966
 Ile Arg Arg Thr Arg Leu Ser Lys Gly Ser
 300 305

10 tagaattgtca ttttacactt cttatcaatg aggaaggggtg atttttgatg tatttgatag 1026
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 35 40 45

40 Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu
 50 55 60

45 Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu

143

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10	Ala	Arg	Lys	Lys	Ser	Glu	Arg	Phe	Thr	Tyr	Leu	Val	Ala	Ala	Ile	Met
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			115					120					125			
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			130				135						140			
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				165					170					175		
35	His	Glu	Ser	His	His	Lys	Pro	Arg	Glu	Gly	Pro	Phe	Glu	Leu	Asn	Asp
			180						185					190		
40	Val	Phe	Ala	Ile	Thr	Asn	Ala	Val	Pro	Ala	Ile	Ala	Leu	Leu	Asn	Tyr
		195						200					205			
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	210						215					220				
50	Leu	Gly	Ile	Thr	Val	Phe	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly
	225					230					235				240	
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				245					250					255		

Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe
 260 265 270

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Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu
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aac tcc aac gga tct ttc cgt tct tat cag cct cgc act tcc gat gac 96
 45 Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp

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	Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser			
5	35	40	45	
	gac gcg ctt cct ctt ccg tta tat ctc aca aac gcc gtt ttc ttc acg			192
	Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr			
	50	55	60	
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	ctc ttc ttc tcc gtc gcg tat tac ctc ctc cac cgg tgg cgt gac aag			240
	Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys			
	65	70	75	80
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	atc cgt tac aat acg cct ctt cac gtc gtc act atc aca gaa ctc ggc			288
	Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly			
	85	90	95	
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	gcc att att gct ctc atc gct tcg ttt atc tat ctc cta ggg ttt ttt			336
	Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe			
	100	105	110	
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	ggc att gac ttt gtt cag tca ttt atc tca cgt gcc tct ggt gat gct			384
	Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala			
	115	120	125	
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	tgg gat ctc gcc gat acg atc gat gat gat gac cac cgc ctt gtc acg			432
	Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr			
	130	135	140	
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	tgc tct cca ccg act ccg atc gtt tcc gtt gct aaa tta cct aat ccg			480
	Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro			
	145	150	155	160
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	gaa cct att gtt acc gaa tcg ctt cct gag gaa gac gag gag att gtg			528
	Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val			
	165	170	175	
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	aaa tcg gtt atc gac gga gtt att cca tcg tac tcg ctt gaa tct cgt			576
	Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg			
	180	185	190	
	ctc ggt gat tgc aaa aga gcg gcg tcg att cgt cgt gag gcg ttg cag			624
	Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln			
	195	200	205	

	aga gtc acc ggg aga tcg att gaa ggg tta ccg ttg gat gga ttt gat	672
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5	tat gaa tcg att ttg ggg caa tgc tgt gag atg cct gtt gga tac att	720
	Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile	
	225 230 235 240	
10	cag att cct gtt ggg att gct ggt cca ttg ttg ctt gat ggt tat gag	768
	Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu	
	245 250 255	
15	tac tct gtt cct atg gct aca acc gaa ggt tgt ttg gtt gct agc act	816
	Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr	
	260 265 270	
20	aac aga ggc tgc aag gct atg ttt atc tct ggt ggc gcc acc agt acc	864
	Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr	
	275 280 285	
25	gtt ctt aag gac ggt atg acc cga gca cct gtt gtt cgg ttc gct tcg	912
	Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser	
	290 295 300	
30	gcg aga cga gct tcg gag ctt aag ttt ttc ttg gag aat cca gag aac	960
	Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn	
	305 310 315 320	
35	ttt gat act ttg gca gta gtc ttc aac agg tcg agt aga ttt gca aga	1008
	Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg	
	325 330 335	
40	ctg caa agt gtt aaa tgc aca atc gcg ggg aag aat gct tat gta agg	1056
	Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg	
	340 345 350	
45	ttc tgt tgt agt act ggt gat gct atg ggg atg aat atg gtt tct aaa	1104
	Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys	
	355 360 365	
50	ggg gtg cag aat gtt ctt gag tat ctt acc gat gat ttc cct gac atg	1152
	Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met	
	370 375 380	

147

	gat	gtg	att	gga	atc	tct	ggt	aac	ttc	tgt	tcg	gac	aag	aaa	cct	gct	1200
	Asp	Val	Ile	Gly	Ile	Ser	Gly	Asn	Phe	Cys	Ser	Asp	Lys	Lys	Pro	Ala	
	385					390					395					400	
5	gct	gtg	aac	tgg	att	gag	gga	cgt	ggt	aaa	tca	ggt	ggt	tgc	gag	gct	1248
	Ala	Val	Asn	Trp	Ile	Glu	Gly	Arg	Gly	Lys	Ser	Val	Val	Cys	Glu	Ala	
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	gta	atc	aga	gga	gag	atc	gtg	aac	aag	gtc	ttg	aaa	acg	agc	gtg	gct	1296
10	Val	Ile	Arg	Gly	Glu	Ile	Val	Asn	Lys	Val	Leu	Lys	Thr	Ser	Val	Ala	
				420					425					430			
	gct	tta	gtc	gag	ctc	aac	atg	ctc	aag	aac	cta	gct	ggc	tct	gct	ggt	1344
15	Ala	Leu	Val	Glu	Leu	Asn	Met	Leu	Lys	Asn	Leu	Ala	Gly	Ser	Ala	Val	
		435						440					445				
	gca	ggc	tct	cta	ggt	gga	ttc	aac	gct	cat	gcc	agt	aac	ata	gtg	tct	1392
	Ala	Gly	Ser	Leu	Gly	Gly	Phe	Asn	Ala	His	Ala	Ser	Asn	Ile	Val	Ser	
		450					455					460					
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	Ala	Val	Phe	Ile	Ala	Thr	Gly	Gln	Asp	Pro	Ala	Gln	Asn	Val	Glu	Ser	
	465					470					475				480		
25	tct	caa	tgc	atc	acc	atg	atg	gaa	gct	att	aat	gac	ggc	aaa	gat	atc	1488
	Ser	Gln	Cys	Ile	Thr	Met	Met	Glu	Ala	Ile	Asn	Asp	Gly	Lys	Asp	Ile	
					485						490				495		
	cat	atc	tca	gtc	act	atg	cca	tct	atc	gag	gtg	ggg	aca	gtg	gga	gga	1536
30	His	Ile	Ser	Val	Thr	Met	Pro	Ser	Ile	Glu	Val	Gly	Thr	Val	Gly	Gly	
				500						505				510			
	gga	aca	cag	ctt	gca	tct	caa	tca	gcg	tgt	tta	aac	ctg	ctc	gga	ggt	1584
35	Gly	Thr	Gln	Leu	Ala	Ser	Gln	Ser	Ala	Cys	Leu	Asn	Leu	Leu	Gly	Val	
		515						520					525				
	aaa	gga	gca	agc	aca	gag	tcg	ccg	gga	atg	aac	gca	agg	agg	cta	gcg	1632
	Lys	Gly	Ala	Ser	Thr	Glu	Ser	Pro	Gly	Met	Asn	Ala	Arg	Arg	Leu	Ala	
		530						535				540					
40	acg	atc	gta	gcc	gga	gca	ggt	tta	gct	gga	gag	tta	tct	tta	atg	tca	1680
	Thr	Ile	Val	Ala	Gly	Ala	Val	Leu	Ala	Gly	Glu	Leu	Ser	Leu	Met	Ser	
	545					550					555				560		
45	gca	att	gca	gct	gga	cag	ctt	gtg	aga	agt	cac	atg	aaa	tac	aat	aga	1728

Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
 565 570 575

tcc agc cga gac atc tct gga gca acg aca acg aca aca aca aca aca 1776
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Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser
 35 40 45

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Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr
 50 55 60

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Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys
 65 70 75 80

Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly
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Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe
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5 Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala
115 120 125

10 Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr
130 135 140

Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro
15 145 150 155 160

Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val
165 170 175

20 Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg
180 185 190

25 Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln
195 200 205

30 Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp
210 215 220

Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile
35 225 230 235 240

Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu
245 250 255

40 Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr
260 265 270

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150

	Asn	Arg	Gly	Cys	Lys	Ala	Met	Phe	Ile	Ser	Gly	Gly	Ala	Thr	Ser	Thr	
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	290							295									300
10	Ala	Arg	Arg	Ala	Ser	Glu	Leu	Lys	Phe	Phe	Leu	Glu	Asn	Pro	Glu	Asn	
	305					310						315				320	
15	Phe	Asp	Thr	Leu	Ala	Val	Val	Phe	Asn	Arg	Ser	Ser	Arg	Phe	Ala	Arg	
					325					330					335		
20	Leu	Gln	Ser	Val	Lys	Cys	Thr	Ile	Ala	Gly	Lys	Asn	Ala	Tyr	Val	Arg	
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30	Gly	Val	Gln	Asn	Val	Leu	Glu	Tyr	Leu	Thr	Asp	Asp	Phe	Pro	Asp	Met	
		370				375						380					
35	Asp	Val	Ile	Gly	Ile	Ser	Gly	Asn	Phe	Cys	Ser	Asp	Lys	Lys	Pro	Ala	
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40	Ala	Val	Asn	Trp	Ile	Glu	Gly	Arg	Gly	Lys	Ser	Val	Val	Cys	Glu	Ala	
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		435						440					445				
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151

450

455

460

Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser
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Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile
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His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly
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15 Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val
 515 520 525

20 Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala
 530 535 540

25 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
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Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
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<211> 1401

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<213> Arabidopsis thaliana ISPH

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<223>

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ttc gtg cgg gag aat cat ctc tct gga tcc gga tct ctc cgc cgc cgg 96
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aaa gct tta tca gtc cgg tgc tcg tct ggc gat gag aac gct cct tcg 144
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cca tcg gtg gtg atg gac tcc gat ttc gac gcc aag gtg ttc cgt aag 192
 Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
 50 55 60

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aac ttg acg aga agc gat aat tac aat cgt aaa ggg ttc ggt cat aag 240
 Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
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gag gag aca ctc aag ctc atg aat cga gag tac acc agt gat ata ttg 288
 Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

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gag aca ctg aaa aca aat ggg tat act tat tct tgg gga gat gtt act 336
 Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
 100 105 110

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gtg aaa ctc gct aaa gca tat ggt ttt tgc tgg ggt gtt gag cgt gct 384
 Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
 115 120 125

gtt cag att gca tat gaa gca cga aag cag ttt cca gag gag agg ctt 432
 Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu

153

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	Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu			
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	gaa gat atg gat gtt aaa att att ccg gtt gag gat tca aag aaa cag			528
	Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln			
		165	170	175
10				
	ttt gat gta gta gag aaa gat gat gtg gtt atc ctt cct gcg ttt gga			576
	Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly			
		180	185	190
	gct ggt gtt gac gag atg tat gtt ctt aat gat aaa aag gtg caa att			624
15	Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile			
		195	200	205
	gtt gac acg act tgt cct tgg gtg aca aag gtc tgg aac acg gtt gag			672
20	Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu			
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	Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn			
25	225	230	235	240
	cat gaa gag acg att gca act gcg tct ttt gca gga aag tac atc att			768
	His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile			
		245	250	255
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	gta aag aac atg aaa gag gca aat tac gtt tgt gat tac att ctc ggt			816
	Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly			
		260	265	270
	ggc caa tac gat gga tct agc tcc aca aaa gag gag ttc atg gag aaa			864
35	Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys			
		275	280	285
	ttc aaa tac gca att tcg aag ggt ttc gat ccc gac aat gac ctt gtc			912
40	Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val			
		290	295	300
	aaa gtt ggt att gca aac caa aca acg atg cta aag gga gaa aca gag			960
	Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu			
45	305	310	315	320

	gag ata gga aga tta ctc gag aca aca atg atg cgc aag tat gga gtg	1008
	Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val	
	325 330 335	
5	gaa aat gta agc gga cat ttc atc agc ttc aac aca ata tgc gac gtt	1056
	Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala	
	340 345 350	
10	act caa gag cga caa gac gca atc tat gag cta gtg gaa gag aag att	1104
	Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile	
	355 360 365	
	gac ctc atg gta gtg gtt ggc gga tgg aat tca agt aac acc tct cac	1152
15	Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His	
	370 375 380	
	ctt cag gaa atc tca gag gca cgg gga atc cca tct tac tgg atc gat	1200
	Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp	
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	agt gag aaa cgg ata gga cct ggg aat aaa ata gcc tat aag ctc cac	1248
	Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His	
	405 410 415	
25	tat gga gaa ctg gtc gag aag gaa aac ttt ctc cca aag gga cca ata	1296
	Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile	
	420 425 430	
30	aca atc ggt gtg aca tca ggt gca tca acc ccg gat aag gtc gtg gaa	1344
	Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu	
	435 440 445	
	gat gct ttg gtg aag gtg ttc gac att aaa cgt gaa gag tta ttg cag	1392
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<211> 466

<212> PRT

5 <213> Arabidopsis thaliana ISPH

<400> 102

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Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser
 35 40 45

25

Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
 50 55 60

30

Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
 65 70 75 80

Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

35

Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
 100 105 110

40

Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
 115 120 125

45

Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu
 130 135 140

Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu
 145 150 155 160

5

Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln
 165 170 175

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Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly
 180 185 190

15

Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile
 195 200 205

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Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu
 210 215 220

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Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn
 225 230 235 240

30

His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile
 245 250 255

35

Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly
 260 265 270

40

Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys
 275 280 285

45

Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val
 290 295 300

Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu
 305 310 315 320

157

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10	Thr	Gln	Glu	Arg	Gln	Asp	Ala	Ile	Tyr	Glu	Leu	Val	Glu	Glu	Lys	Ile	
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15	Asp	Leu	Met	Leu	Val	Val	Gly	Gly	Trp	Asn	Ser	Ser	Asn	Thr	Ser	His	
					370					375					380		
20	Leu	Gln	Glu	Ile	Ser	Glu	Ala	Arg	Gly	Ile	Pro	Ser	Tyr	Trp	Ile	Asp	
					385					390					395		400
25	Ser	Glu	Lys	Arg	Ile	Gly	Pro	Gly	Asn	Lys	Ile	Ala	Tyr	Lys	Leu	His	
					405					410					415		
30	Tyr	Gly	Glu	Leu	Val	Glu	Lys	Glu	Asn	Phe	Leu	Pro	Lys	Gly	Pro	Ile	
					420					425					430		
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gtg gtt tca gat tct tct aag gca acc cct ttg ttc tct gga tgg att 96
 Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile
 20 25 30

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cat gga aca gat ctg cag ttt ttg ttc caa cac aag ctt act cat gag 144
 His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
 35 40 45

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gtc aag aaa agg tca cgt gtg gtt cag gct tcc tta tca gaa tct gga 192
 Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
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gaa tac tac aca cag aga ccg cca acg cct att ttg gac act gtg aac 240
 Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
 65 70 75 80

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tat ccc att cat atg aaa aat ctg tct ctg aag gaa ctt aaa caa cta 288
 Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
 85 90 95

gca gat gaa cta agg tca gat aca att ttc aat gta tca aag act ggg 336
 Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
 100 105 110

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	ggt cac ctt ggc tca agt ctt ggt gtt ggt gag ctg act gtt gct ctt	384
	Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu	
	115 120 125	
5	cat tat gtc ttc aat gca ccg caa gat agg att ctc tgg gat gtt ggt	432
	His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly	
	130 135 140	
10	cat cag tct tat cct cac aaa atc ttg act ggt aga agg gac aag atg	480
	His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met	
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	Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser	
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20	gag agt gaa tat gat tgc ttt ggc acc ggc cac agt tcc acc acc atc	576
	Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile	
	180 185 190	
25	tca gca ggc cta ggg atg gct gtt ggt aga gat cta aaa gga aga aac	624
	Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn	
	195 200 205	
30	aac aat gtt att gcc gta ata ggt gat ggt gcc atg aca gca ggt caa	672
	Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln	
	210 215 220	
35	gct tat gaa gcc atg aat aat gct ggt tac ctg gac tct gac atg att	720
	Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile	
	225 230 235 240	
40	ggt atc tta aac gac aat aga caa gtt tct tta cct act gct act ctg	768
	Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu	
	245 250 255	
45	gat ggg cca gtt gct cct gtt gga gct cta agt agt gct ttg agc agg	816
	Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg	
	260 265 270	
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	Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly	
	275 280 285	
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160

	Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val	
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	305 310 315 320	
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	325 330 335	
15	gat gat cta att gcg att ctc aaa gag gtt aga agt act aaa aca aca Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr	1056
	340 345 350	
	ggg cca gta ctg atc cat gtt gtc act gag aaa ggc aga ggt tat cca Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro	1104
	355 360 365	
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	370 375 380	
25	cca gca aca gga aag caa ttc aaa gcc agt gcc aag aca cag tcc tat Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr	1200
	385 390 395 400	
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	405 410 415	
35	gac att gtt gca atc cat gct gcc atg ggg ggt ggg acc gga atg aac Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn	1296
	420 425 430	
	ctt ttc cat cgt cgc ttc cca aca agg tgt ttt gat gtt gga ata gca Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala	1344
	435 440 445	
40	gaa caa cat gca gta acc ttt gct gct gga ttg gct tgt gaa ggc att Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile	1392
	450 455 460	
45	aaa cct ttc tgt gca atc tat tcg tct ttc atg cag agg gct tat gac Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp	1440

161

	465	470	475	480	
	cag gta gtg cat gac gtt gat ttg caa aag ctg ccc gtg agg ttt gca				1488
	Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala				
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	atg gac aga gca ggt ctt gtt gga gca gat ggt cca aca cat tgt ggt				1536
	Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly				
		500	505	510	
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	gca ttt gat gtt act tac atg gca tgt ctt cct aac atg gtt gta atg				1584
	Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met				
		515	520	525	
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	gct cct tct gat gaa gcg gag cta ttt cac atg gta gca act gct gcc				1632
	Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala				
		530	535	540	
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	gcc att gat gac aga cca agt tgt ttt aga tac cca aga gga aat ggg				1680
	Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly				
		545	550	555	560
	atc ggt gta gag ctt ccg gct gga aac aaa gga att cct ctt gag gtt				1728
	Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val				
25		565	570	575	
	ggt aaa ggt agg ata ttg att gag ggg gag aga gtg gct cta ttg gga				1776
	Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly				
		580	585	590	
30					
	tat ggc tca gca gtg cag aac tgt ttg gat gct gct att gtg cta gaa				1824
	Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu				
		595	600	605	
35					
	tcc cgc ggc tta caa gta aca gtt gca gat gca cgt ttc tgc aaa cca				1872
	Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro				
		610	615	620	
40					
	ctg gac cat gcc ctc ata agg agc ctt gca aaa tca cat gaa gtg cta				1920
	Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu				
		625	630	635	640
	atc act gtc gaa gaa gga tca att gga ggt ttt gga tct cat gtt gtt				1968
	Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val				
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5 cag ttc atg gcc tta gat ggg ctt ctt gat ggc aag ttg aag tgg aga 2016
 Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
 660 665 670

10 cca ata gtt ctt cct gat cga tac att gac cat gga tct cct gtt gat 2064
 Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
 675 680 685

15 cag ttg gcg gaa gct ggc cta aca cca tct cac att gca gca aca gta 2112
 Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
 690 695 700

20 ttt aac ata ctt gga caa acc aga gag gct cta gag gtc atg aca taa 2160
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40 His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
 35 40 45

45 Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
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Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
 65 70 75 80

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Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
 85 90 95

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Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
 100 105 110

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Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu
 115 120 125

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His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly
 130 135 140

His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met
 145 150 155 160

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Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser
 165 170 175

30

Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile
 180 185 190

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Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn
 195 200 205

40

Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln
 210 215 220

Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile
 225 230 235 240

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164

	Val	Ile	Leu	Asn	Asp	Asn	Arg	Gln	Val	Ser	Leu	Pro	Thr	Ala	Thr	Leu	
					245					250						255	
5	Asp	Gly	Pro	Val	Ala	Pro	Val	Gly	Ala	Leu	Ser	Ser	Ala	Leu	Ser	Arg	
					260				265					270			
10	Leu	Gln	Ser	Asn	Arg	Pro	Leu	Arg	Glu	Leu	Arg	Glu	Val	Ala	Lys	Gly	
				275				280					285				
15	Val	Thr	Lys	Gln	Ile	Gly	Gly	Pro	Met	His	Glu	Leu	Ala	Ala	Lys	Val	
		290				295						300					
20	Asp	Glu	Tyr	Ala	Arg	Gly	Met	Ile	Ser	Gly	Ser	Gly	Ser	Thr	Leu	Phe	
	305					310					315					320	
25	Glu	Glu	Leu	Gly	Leu	Tyr	Tyr	Ile	Gly	Pro	Val	Asp	Gly	His	Asn	Ile	
				325						330				335			
30	Asp	Asp	Leu	Ile	Ala	Ile	Leu	Lys	Glu	Val	Arg	Ser	Thr	Lys	Thr	Thr	
				340					345					350			
35	Gly	Pro	Val	Leu	Ile	His	Val	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Pro	
		355					360						365				
40	Tyr	Ala	Glu	Arg	Ala	Ala	Asp	Lys	Tyr	His	Gly	Val	Ala	Lys	Phe	Asp	
	370						375					380					
45	Pro	Ala	Thr	Gly	Lys	Gln	Phe	Lys	Ala	Ser	Ala	Lys	Thr	Gln	Ser	Tyr	
	385				390					395					400		
50	Thr	Thr	Tyr	Phe	Ala	Glu	Ala	Leu	Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys	
				405					410					415			
55	Asp	Ile	Val	Ala	Ile	His	Ala	Ala	Met	Gly	Gly	Gly	Thr	Gly	Met	Asn	

420

425

430

5 Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala
435 440 445

10 Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile
450 455 460

15 Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp
465 470 475 480

Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala
485 490 495

20 Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly
500 505 510

25 Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met
515 520 525

30 Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala
530 535 540

35 Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly
545 550 555 560

Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val
565 570 575

40 Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly
580 585 590

45 Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu
595 600 605

Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro
 610 615 620

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Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu
 625 630 635 640

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Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val
 645 650 655

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Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
 660 665 670

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Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
 675 680 685

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Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
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Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr
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	145	150	155	160	
	gag caa gga gtg att gag gtt gcc cga cat cct gaa gct gta acc gtt				528
	Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val				
5		165	170	175	
	gtt acc gga ata gta ggt tgt gcg gga cta aag cct acg gtt gct gca				576
	Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala				
		180	185	190	
10	att gaa gca gga aag gac att gct ctt gca aac aaa gag aca tta atc				624
	Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile				
		195	200	205	
15	gca ggt ggt cct ttc gtg ctt ccg ctt gcc aac aaa cat aat gta aag				672
	Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys				
		210	215	220	
	att ctt ccg gca gat tca gaa cat tct gcc ata ttt cag tgt att caa				720
20	Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln				
		225	230	235	240
	ggt ttg cct gaa ggc gct ctg cgc aag ata atc ttg act gca tct ggt				768
	Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly				
25		245	250	255	
	gga gct ttt agg gat tgg cct gtc gaa aag cta aag gaa gtt aaa gta				816
	Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val				
		260	265	270	
30	gcg gat gcg ttg aag cat cca aac tgg aac atg gga aag aaa atc act				864
	Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr				
		275	280	285	
35	gtg gac tct gct acg ctt ttc aac aag ggt ctt gag gtc att gaa gcg				912
	Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala				
		290	295	300	
	cat tat ttg ttt gga gct gag tat gac gat ata gag att gtc att cat				960
40	His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His				
		305	310	315	320
	ccg caa agt atc ata cat tcc atg att gaa aca cag gat tca tct gtg				1008
	Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val				
45		325	330	335	

	ctt gct caa ttg ggt tgg cct gat atg cgt tta ccg att ctc tac acc	1056
	Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr	
	340 345 350	
5	atg tca tgg ccc gat aga gtt cct tgt tct gaa gta act tgg cca aga	1104
	Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg	
	355 360 365	
10	ctt gac ctt tgc aaa ctc ggt tca ttg act ttc aag aaa cca gac aat	1152
	Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn	
	370 375 380	
	gtg aaa tac cca tcc atg gat ctt gct tat gct gct gga cga gct gga	1200
15	Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly	
	385 390 395 400	
	ggc aca atg act gga gtt ctc agc gcc gcc aat gag aaa gct gtt gaa	1248
	Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu	
20	405 410 415	
	atg ttc att gat gaa aag ata agc tat ttg gat atc ttc aag gtt gtg	1296
	Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val	
	420 425 430	
25	gaa tta aca tgc gat aaa cat cga aac gag ttg gta aca tca ccg tct	1344
	Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser	
	435 440 445	
30	ctt gaa gag att gtt cac tat gac ttg tgg gca cgt gaa tat gcc gcg	1392
	Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala	
	450 455 460	
	aat gtg cag ctt tct tct ggt gct agg cca gtt cat gca tga	1434
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Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val

35

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Lys Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp

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55

60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro

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75

80

25

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr

85

90

95

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Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu

100

105

110

35

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe

115

120

125

40

Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu

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135

140

Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly

145

150

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160

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Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
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5 Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
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10 Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 195 200 205

15 Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
 210 215 220

20 Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
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Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
 245 250 255

25 Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
 260 265 270

30 Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
 275 280 285

35 Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
 290 295 300

40 His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
 305 310 315 320

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
 325 330 335

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Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
 340 345 350

5 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
 355 360 365

10 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
 370 375 380

15 Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
 385 390 395 400

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
 405 410 415

20 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
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25 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
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<211> 884

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5 <221> CDS

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cttccatcac taacagtcct cgccgagggg tgaatcggtt gttcgcctca acgtcgact 179

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atg ggt gaa gtc gct gat gct ggt atg gat gcc gtc cag aag cgg ctt 227

Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu

1 5 10 15

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Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val

20 25 30

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gga cat gat tcc aaa tac aac tgt cat ttg atg gaa aag ata gag gca 323

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala

35 40 45

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gaa aac ttg ctt cac aga gcc ttc agt gtt ttc tta ttc aac tca aaa 371

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys

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tac gag ttg ctt ctt cag caa cga tct gca acg aag gta aca ttc ccg 419

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro

65 70 75 80

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ctc gta tgg aca aac acc tgt tgc agc cat ccc ctc ttc cgt gat tcc 467

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser

85 90 95

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gaa ctc ata gaa gaa aat ttt ctc ggg gta cga aac gct gca caa agg 515

Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg

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	Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp			
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	gaa ttc act cct ctt ggt cgc att ctt tac aaa gct cca tct gac gga			611
	Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly			
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	Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp			
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15	gtg aaa tac gat cca aac cca gat gaa gtt gct gac gct aag tac gtt			707
	Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val			
		165	170	175
	aat cgc gag gag ttg aaa gag ata ctg aga aaa gct gat gca ggt gaa			755
20	Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu			
		180	185	190
	gag gga ata aag ttg tct cct tgg ttt aga ttg gtt gtg gat aac ttt			803
	Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe			
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	ttg ttc aag tgg tgg gat cat gta gag gag ggg aag att aag gac gtc			851
	Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val			
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 35 40 45
 15 Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60
 20 Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80
 Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
 85 90 95
 25 Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110
 30 Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125
 35 Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140
 Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 40 145 150 155 160
 Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
 165 170 175
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176

Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
 180 185 190

5

Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205

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Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val
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 Phe Thr Arg Ser Val Ala Arg Ile Ser Ser Lys Phe Leu Arg Asn Arg

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	Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe Ala Ile	
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5	att ccc gat cag ggt cac tct tgt tct gac tct cca cac aag ggt tac	201
	Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys Gly Tyr	
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10	gtt tgc aga aca act tat tca ttg aaa tct ccg gtt ttt ggt gga ttt	249
	Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly Gly Phe	
	55 60 65	
15	agt cat caa ctc tat cac cag agt agc tcc ttg gtt gag gag gag ctt	297
	Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu Glu Leu	
	70 75 80	
20	gac cca ttt tcg ctt gtt gcc gat gag ctg tca ctt ctt agt aat aag	345
	Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser Asn Lys	
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	Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser Ala Ala	
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	Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg Ser Thr	
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35	att ttg ctg ctg atg gcg aca gct ctg gat gta cga gtt cca gaa gca	489
	Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro Glu Ala	
	135 140 145	
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	Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu	
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50	ctg cac gat gat gtc ttg gat gat gcc gat aca agg cgt ggt gtt ggt	633
	Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly	
	180 185 190	

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	Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr	
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10	gag gtt gta gca tta ctt gca act gct gta gaa cat ctt gtt acc ggt	777
	Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly	
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15	gaa acc atg gag ata act agt tca acc gag cag cgt tat agt atg gac	825
	Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp	
	245 250 255	
20	tac tac atg cag aag aca tat tat aag aca gca tcg cta atc tct aac	873
	Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn	
	260 265 270	
	agc tgc aaa gct ggt gcc gtt ctc act gga caa aca gca gaa gtt gcc	921
	Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala	
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	Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu	
	295 300 305	
30	ata gac gac att ctt gat ttc acg ggc aca tct gcc tct ctc gga aag	1017
	Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys	
	310 315 320	
35	gga tcg ttg tca gat att cgc cat gga gtc ata aca gcc cca atc ctc	1065
	Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu	
	325 330 335	
40	ttt gcc atg gaa gag ttt cct caa cta cgc gaa gtt gtt gat caa gtt	1113
	Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val	
	340 345 350	
	gaa aaa gat cct agg aat gtt gac att gct tta gag tat ctt ggg aag	1161
	Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys	
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45	agc aag gga ata cag agg gca aga gaa tta gcc atg gaa cat gcg aat	1209

179

Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn
 375 380 385

cta gca gca gct gca atc ggg tct cta cct gaa aca gac aat gaa gat 1257
 5 Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp
 390 395 400

gtc aaa aga tcg agg cgg gca ctt att gac ttg acc cat aga gtc atc 1305
 10 Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile
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acc aga aac aag tgagattaag taatgtttct ctctatacac caaaacattc 1357
 Thr Arg Asn Lys
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40 Ala Ile Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys
 35 40 45

45 Gly Tyr Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly
 50 55 60

Gly Phe Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu
 65 70 75 80

5

Glu Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser
 85 90 95

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Asn Lys Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser
 100 105 110

15

Ala Ala Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg
 115 120 125

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Ser Thr Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro
 130 135 140

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Glu Ala Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg
 145 150 155 160

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Val Arg Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala
 165 170 175

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Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly
 180 185 190

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Val Gly Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala
 195 200 205

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Gly Asp Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys
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Asn Thr Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val
 225 230 235 240

181

Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser
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5 Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile
 260 265 270

10 Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu
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Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu
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20 Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro
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25 Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp
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30 Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu
 355 360 365

35 Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His
 370 375 380

Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn
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45 Val Ile Thr Arg Asn Lys

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 gca ata cct tca cat cat ttg cat ctg aga agt ctt ggt ggg agt ctc 96
 30 Ala Ile Pro Ser His His Leu His Leu Arg Ser Leu Gly Gly Ser Leu
 20 25 30
 tat cgt cgt cgt atc caa agc tct tca atg gag acc gat ctc aag tca 144
 35 Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser
 35 40 45
 acc ttt ctc aac gtt tat tct gtt ctc aag tct gac ctt ctt cat gac 192
 40 Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp
 50 55 60
 cct tcc ttc gaa ttc acc aat gaa tct cgt ctc tgg gtt gat cgg atg 240
 Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met
 65 70 75 80
 45 ctg gac tac aat gta cgt gga ggg aaa ctc aat cgg ggt ctc tct gtt 288

183

	Leu	Asp	Tyr	Asn	Val	Arg	Gly	Gly	Lys	Leu	Asn	Arg	Gly	Leu	Ser	Val	
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5	ggt	gac	agt	ttc	aaa	ctt	ttg	aag	caa	ggc	aat	gat	ttg	act	gag	caa	336
	Val	Asp	Ser	Phe	Lys	Leu	Leu	Lys	Gln	Gly	Asn	Asp	Leu	Thr	Glu	Gln	
				100					105				110				
10	gag	ggt	ttc	ctc	tct	tgt	gct	ctc	ggg	tgg	tgc	att	gaa	tgg	ctc	caa	384
	Glu	Val	Phe	Leu	Ser	Cys	Ala	Leu	Gly	Trp	Cys	Ile	Glu	Trp	Leu	Gln	
				115				120					125				
15	gct	tat	ttc	ctt	gtg	ctt	gat	gat	att	atg	gat	aac	tct	gtc	act	cgc	432
	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met	Asp	Asn	Ser	Val	Thr	Arg	
				130				135					140				
20	cgt	ggg	caa	cct	tgc	tgg	ttc	aga	ggt	cct	cag	ggt	ggt	atg	ggt	gcc	480
	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro	Gln	Val	Gly	Met	Val	Ala	
				145				150				155		160			
25	atc	aat	gat	ggg	att	cta	ctt	cgc	aat	cac	atc	cac	agg	att	ctc	aaa	528
	Ile	Asn	Asp	Gly	Ile	Leu	Leu	Arg	Asn	His	Ile	His	Arg	Ile	Leu	Lys	
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30	aag	cat	ttc	cgt	gat	aag	cct	tac	tat	ggt	gac	ctt	ggt	gat	ttg	ttt	576
	Lys	His	Phe	Arg	Asp	Lys	Pro	Tyr	Tyr	Val	Asp	Leu	Val	Asp	Leu	Phe	
				180				185					190				
35	aat	gag	ggt	gag	ttg	caa	aca	gct	tgt	ggc	cag	atg	ata	gat	ttg	atc	624
	Asn	Glu	Val	Glu	Leu	Gln	Thr	Ala	Cys	Gly	Gln	Met	Ile	Asp	Leu	Ile	
				195				200					205				
40	acc	acc	ttt	gaa	gga	gaa	aag	gat	ttg	gcc	aag	tac	tca	ttg	tca	atc	672
	Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile	
				210				215				220					
45	cac	cgt	cgt	att	gtc	cag	tac	aaa	acg	gct	tat	tac	tca	ttt	tat	ctc	720
	His	Arg	Arg	Ile	Val	Gln	Tyr	Lys	Thr	Ala	Tyr	Tyr	Ser	Phe	Tyr	Leu	
				225				230				235		240			
50	cct	ggt	gct	tgt	gcg	ttg	ctt	atg	gcg	ggc	gaa	aat	ttg	gaa	aac	cat	768
	Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His	
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55	att	gac	gtg	aaa	aat	ggt	ctt	ggt	gac	atg	gga	atc	tac	ttc	caa	gtg	816
	Ile	Asp	Val	Lys	Asn	Val	Leu	Val	Asp	Met	Gly	Ile	Tyr	Phe	Gln	Val	

	260	265	270	
	cag gat gat tat ctg gat tgt ttt gct gat ccc gag acg ctt ggc aag			864
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	ata gga aca gat ata gaa gat ttc aaa tgc tcg tgg ttg gtg gtt aag			912
	Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys			
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	Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn			
	305	310	315	320
15	tat ggt aaa ccc gac cca tcg aac gtt gct aaa gtg aag gat ctc tac			1008
	Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr			
	325	330	335	
20	aaa gag ctg gat ctt gag gga gtt ttc atg gag tat gag agc aaa agc			1056
	Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser			
	340	345	350	
	tac gag aag ctg act gga gcg att gag gga cac caa agt aaa gca atc			1104
	Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile			
25	355	360	365	
	caa gca gtg cta aaa tcc ttc ttg gct aag atc tac aag agg cag aag			1152
	Gln Ala Val Leu Lys Ser Phe Leu Ala Lys Ile Tyr Lys Arg Gln Lys			
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	tag			1155
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185

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5	Ala	Ile	Pro	Ser	His	His	Leu	His	Leu	Arg	Ser	Leu	Gly	Gly	Ser	Leu	
					20				25					30			
10	Tyr	Arg	Arg	Arg	Ile	Gln	Ser	Ser	Ser	Met	Glu	Thr	Asp	Leu	Lys	Ser	
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		50					55					60					
20	Pro	Ser	Phe	Glu	Phe	Thr	Asn	Glu	Ser	Arg	Leu	Trp	Val	Asp	Arg	Met	
	65					70					75					80	
25	Leu	Asp	Tyr	Asn	Val	Arg	Gly	Gly	Lys	Leu	Asn	Arg	Gly	Leu	Ser	Val	
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30	Val	Asp	Ser	Phe	Lys	Leu	Leu	Lys	Gln	Gly	Asn	Asp	Leu	Thr	Glu	Gln	
				100					105					110			
35	Glu	Val	Phe	Leu	Ser	Cys	Ala	Leu	Gly	Trp	Cys	Ile	Glu	Trp	Leu	Gln	
			115					120					125				
40	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met	Asp	Asn	Ser	Val	Thr	Arg	
		130					135					140					
45	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro	Gln	Val	Gly	Met	Val	Ala	
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					165				170					175			
55	Lys	His	Phe	Arg	Asp	Lys	Pro	Tyr	Tyr	Val	Asp	Leu	Val	Asp	Leu	Phe	

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10	Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile	210	215	220
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20	Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His	245	250	255
25	Ile	Asp	Val	Lys	Asn	Val	Leu	Val	Asp	Met	Gly	Ile	Tyr	Phe	Gln	Val	260	265	270
30	Gln	Asp	Asp	Tyr	Leu	Asp	Cys	Phe	Ala	Asp	Pro	Glu	Thr	Leu	Gly	Lys	275	280	285
35	Ile	Gly	Thr	Asp	Ile	Glu	Asp	Phe	Lys	Cys	Ser	Trp	Leu	Val	Val	Lys	290	295	300
40	Ala	Leu	Glu	Arg	Cys	Ser	Glu	Glu	Gln	Thr	Lys	Ile	Leu	Tyr	Glu	Asn	305	310	315 320
45	Tyr	Gly	Lys	Pro	Asp	Pro	Ser	Asn	Val	Ala	Lys	Val	Lys	Asp	Leu	Tyr	325	330	335
50	Lys	Glu	Leu	Asp	Leu	Glu	Gly	Val	Phe	Met	Glu	Tyr	Glu	Ser	Lys	Ser	340	345	350
55	Tyr	Glu	Lys	Leu	Thr	Gly	Ala	Ile	Glu	Gly	His	Gln	Ser	Lys	Ala	Ile	355	360	365

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cat cct tca act atc tta acc caa tcc aga tcc aga tct cct cct tct 96
 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
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ctc atc acc ctt aaa ccc atc tcc ctc act cca aaa cgc acc gtt tcg 144
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
 35 40 45

40

tct tct tcc tcc tct tcc ctc atc acc aaa gaa gac aac aac ctc aaa 192
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 50 55 60

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ctc aag atc cac gaa gcg atg cgt tac tct ctc ctc gcc gga gga aaa	336		
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cgc gtc aga cca gtt ctc tgc atc gcc gcg tgc gag cta gtc gga gga	384		
Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly			
	115	120	125
15			
gaa gag tct tta gct atg ccg gcg cgt tgc gcc gtg gaa atg atc cac	432		
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	130	135	140
20			
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Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp			
	145	150	155
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ctc cgc cgc gga aag ccc acg aat cac aaa gtt tac ggc gaa gac gtg	528		
Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val			
	165	170	175
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gcg gtt tta gcc gga gac gcg ctt ctt tcg ttc gcc ttc gag cat tta	576		
Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu			
	180	185	190
35			
gcg tcg gct acg agc tcg gag gtt tct ccg gcg aga gtg gtt aga gct	624		
Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala			
	195	200	205
40			
gtg gga gag ttg gct aaa gcc atc ggc acc gaa ggg ctc gtg gcg gga	672		
Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly			
	210	215	220
45			
caa gtg gtg gat ata agc agt gaa ggg ttg gac tta aac aac gtc gga	720		
Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly			
	225	230	235
45			
ttg gag cat ttg aag ttt ata cat ttg cat aaa acg gcg gcg ttg ctt	768		
Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu			
	245	250	255

	gaa gct tca gcg gtt ttg ggt ggg atc atc ggt gga ggg agt gat gaa	816
	Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu	
	260 265 270	
5		
	gag atc gag agg ctg agg aag ttc gcg agg tgt att ggg ttg ttg ttt	864
	Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe	
	275 280 285	
10		
	cag gtg gtt gat gat atc ttg gac gtg acg aaa tcg tct caa gaa ctg	912
	Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu	
	290 295 300	
	ggg aaa acc gct ggg aaa gat ttg att gct gat aag ttg act tat ccg	960
15	Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro	
	305 310 315 320	
	aag ctc atg ggt ttg gag aaa tcg aga gag ttc gct gag aag ttg aat	1008
20	Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn	
	325 330 335	
	aca gag gca cgt gat cag ctt tta ggg ttt gat tcc gac aag gtt gct	1056
	Thr Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp Ser Asp Lys Val Ala	
	340 345 350	
25		
	cct ttg ttg gct ttg gct aat tac att gcc aat aga cag aac tga	1101
	Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Asn Arg Gln Asn	
	355 360 365	
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	<210> 114	
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	<212> PRT	
	<213> Sinapis alba	
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	<400> 114	
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His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
 20 25 30

5
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
 35 40 45

10 Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys
 50 55 60

15 Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala
 65 70 75 80

Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro
 85 90 95

20
 Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
 100 105 110

25
 Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly
 115 120 125

30 Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His
 130 135 140

35 Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp
 145 150 155 160

Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val
 165 170 175

40
 Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu
 180 185 190

45

191

	Ala	Ser	Ala	Thr	Ser	Ser	Glu	Val	Ser	Pro	Ala	Arg	Val	Val	Arg	Ala	
			195					200					205				
5	Val	Gly	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Thr	Glu	Gly	Leu	Val	Ala	Gly	
		210					215					220					
10	Gln	Val	Val	Asp	Ile	Ser	Ser	Glu	Gly	Leu	Asp	Leu	Asn	Asn	Val	Gly	
	225					230					235				240		
15	Leu	Glu	His	Leu	Lys	Phe	Ile	His	Leu	His	Lys	Thr	Ala	Ala	Leu	Leu	
					245					250					255		
20	Glu	Ala	Ser	Ala	Val	Leu	Gly	Gly	Ile	Ile	Gly	Gly	Gly	Ser	Asp	Glu	
				260					265					270			
25	Gln	Val	Val	Asp	Asp	Ile	Leu	Asp	Val	Thr	Lys	Ser	Ser	Gln	Glu	Leu	
		290					295					300					
30	Gly	Lys	Thr	Ala	Gly	Lys	Asp	Leu	Ile	Ala	Asp	Lys	Leu	Thr	Tyr	Pro	
	305					310					315				320		
35	Lys	Leu	Met	Gly	Leu	Glu	Lys	Ser	Arg	Glu	Phe	Ala	Glu	Lys	Leu	Asn	
					325					330				335			
40	Thr	Glu	Ala	Arg	Asp	Gln	Leu	Leu	Gly	Phe	Asp	Ser	Asp	Lys	Val	Ala	
				340					345					350			
	Pro	Leu	Leu	Ala	Leu	Ala	Asn	Tyr	Ile	Ala	Asn	Arg	Gln	Asn			
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 Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val
 1 5 10 15
 25
 ggc tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc 96
 Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr
 20 25 30
 30
 cgg cgc agc gta ctg atg ctc tac gcc tgg tgc cgc cat tgt gac gat 144
 Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp
 35 40 45
 35
 gtt att gac gat cag acg ctg ggc ttt cag gcc cgg cag cct gcc tta 192
 Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu
 50 55 60
 40
 caa acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag 240
 Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
 65 70 75 80
 45
 gcc tat gca gga tcg cag atg cac gaa ccg gcg ttt gcg gct ttt cag 288
 Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln
 85 90 95

193

	gaa gtg gct atg gct cat gat atc gcc ccg gct tac gcg ttt gat cat	336
	Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His	
	100 105 110	
5	ctg gaa ggc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg	384
	Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu	
	115 120 125	
10	gat gat acg ctg cgc tat tgc tat cac gtt gca ggc gtt gtc ggc ttg	432
	Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu	
	130 135 140	
15	atg atg gcg caa atc atg ggc gtg cgg gat aac gcc acg ctg gac cgc	480
	Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg	
	145 150 155 160	
20	gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc gat	528
	Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp	
	165 170 175	
	att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca agc tgg	576
	Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp	
	180 185 190	
25	ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca cct gaa aac	624
	Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn	
	195 200 205	
30	cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg cag gaa gca gaa	672
	Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu	
	210 215 220	
35	cct tac tat ttg tct gcc aca gcc ggc ctg gca ggg ttg ccc ctg cgt	720
	Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg	
	225 230 235 240	
40	tcc gcc tgg gca atc gct acg gcg aag cag gtt tac cgg aaa ata ggt	768
	Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly	
	245 250 255	
	gtc aaa gtt gaa cag gcc ggt cag caa gcc tgg gat cag cgg cag tca	816
	Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser	
	260 265 270	
45	acg acc acg ccc gaa aaa tta acg ctg ctg ctg gcc gcc tct ggt cag	864

194

Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
 275 280 285

gcc ctt act tcc cgg atg cgg gct cat cct ccc cgc cct gcg cat ctc 912
 5 Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
 290 295 300

tgg cag cgc ccg ctc tag 930
 Trp Gln Arg Pro Leu
 10 305

<210> 116

15 <211> 309

<212> PRT

<213> Erwinia uredovora
 20

<400> 116

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 1 5 10 15

Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr
 30 20 25 30

Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp
 35 40 45

Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu
 50 55 60

40 Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
 65 70 75 80

45 Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln

195

	85	90	95
5	Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His		
	100	105	110
10	Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu		
	115	120	125
15	Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu		
	130	135	140
20	Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg		
	145	150	155
25	Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp		
	165	170	175
30	Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp		
	180	185	190
35	Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn		
	195	200	205
40	Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu		
	210	215	220
45	Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg		
	225	230	235
50	Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly		
	245	250	255
55	Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser		
	260	265	270

Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
 275 280 285
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Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
 290 295 300

10 Trp Gln Arg Pro Leu
 305

15 <210> 117
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 20 <213> Erwinia ureidovora

25 <220>
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 30 <223>

35 <400> 117
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 Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
 1 5 10 15

40 gca att cgt cta caa gct gcg ggg atc ccc gtc tta ctg ctt gaa caa 96
 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

45 cgt gat aaa ccc ggc ggt cgg gct tat gtc tac gag gat cag ggg ttt 144
 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe

	35		40		45	
	acc ttt gat gca ggc ccg acg gtt atc acc gat ccc agt gcc att gaa	192				
	Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu					
5	50 55 60					
	gaa ctg ttt gca ctg gca gga aaa cag tta aaa gag tat gtc gaa ctg	240				
	Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu					
	65 70 75 80					
10						
	ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg gag tca ggg aag gtc	288				
	Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val					
	85 90 95					
15						
	ttt aat tac gat aac gat caa acc cgg ctc gaa gcg cag att cag cag	336				
	Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln					
	100 105 110					
	ttt aat ccc cgc gat gtc gaa ggt tat cgt cag ttt ctg gac tat tca	384				
20	Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser					
	115 120 125					
	cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc ggt act gtc cct ttt	432				
	Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe					
25	130 135 140					
	tta tcg ttc aga gac atg ctt cgc gcc gca cct caa ctg gcg aaa ctg	480				
	Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu					
	145 150 155 160					
30						
	cag gca tgg aga agc gtt tac agt aag gtt gcc agt tac atc gaa gat	528				
	Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp					
	165 170 175					
35						
	gaa cat ctg cgc cag gcg ttt tct ttc cac tcg ctg ttg gtg ggc ggc	576				
	Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly					
	180 185 190					
	aat ccc ttc gcc acc tca tcc att tat acg ttg ata cac gcg ctg gag	624				
40	Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu					
	195 200 205					
	cgt gag tgg ggc gtc tgg ttt ccg cgt ggc ggc acc ggc gca tta gtt	672				
	Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val					
45	210 215 220					

	cag ggg atg ata aag ctg ttt cag gat ctg ggt ggc gaa gtc gtg tta Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu 225 230 235 240	720
5	aac gcc aga gtc agc cat atg gaa acg aca gga aac aag att gaa gcc Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala 245 250 255	768
10	gtg cat tta gag gac ggt cgc agg ttc ctg acg caa gcc gtc gcg tca Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser 260 265 270	816
15	aat gca gat gtg gtt cat acc tat cgc gac ctg tta agc cag cac cct Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro 275 280 285	864
20	gcc gcg gtt aag cag tcc aac aaa ctg cag act aag cgc atg agt aac Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn 290 295 300	912
25	tct ctg ttt gtg ctc tat ttt ggt ttg aat cac cat cat gat cag ctc Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu 305 310 315 320	960
	gcg cat cac acg gtt tgt ttc ggc ccg cgt tac cgc gag ctg att gac Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp 325 330 335	1008
30	gaa att ttt aat cat gat ggc ctc gca gag gac ttc tca ctt tat ctg Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu 340 345 350	1056
35	cac gcg ccc tgt gtc acg gat tcg tca ctg gcg cct gaa ggt tgc ggc His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly 355 360 365	1104
40	agt tac tat gtg ttg gcg ccg gtg ccg cat tta ggc acc gcg aac ctc Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu 370 375 380	1152
45	gac tgg acg gtt gag ggg cca aaa cta cgc gac cgt att ttt gcg tac Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr 385 390 395 400	1200

ctt gag cag cat tac atg cct ggc tta cgg agt cag ctg gtc acg cac 1248
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415

5 cgg atg ttt acg ccg ttt gat ttt cgc gac cag ctt aat gcc tat cat 1296
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430

10 ggc tca gcc ttt tct gtg gag ccc gtt ctt acc cag agc gcc tgg ttt 1344
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445

15 cgg ccg cat aac cgc gat aaa acc att act aat ctc tac ctg gtc ggc 1392
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460

20 gca ggc acg cat ccc ggc gca ggc att cct ggc gtc atc ggc tcg gca 1440
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480

aaa gcg aca gca ggt ttg atg ctg gag gat ctg ata tga 1479
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

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 <210> 118
 <211> 492

30 <212> PRT
 <213> Erwinia uredovora

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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
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40
 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

45

200

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
 35 40 45

5 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60

10 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu
 65 70 75 80

15 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95

Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
 100 105 110

20 Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125

25 Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
 130 135 140

30 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160

35 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175

40 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
 180 185 190

45 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
 195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val

	210		215		220
5	Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu				
	225		230		235 240
10	Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala				
		245		250	255
	Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser				
		260		265	270
15	Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro				
		275		280	285
20	Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn				
		290		295	300
25	Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu				
		305		315	320
30	Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp				
		325		330	335
	Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu				
		340		345	350
35	His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly				
		355		360	365
40	Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu				
		370		375	380
45	Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr				
		385		395	400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415

5

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430

10

Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445

15

Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460

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Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

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<210> 119

<211> 1725

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<212> DNA

<213> Narcissus pseudonarcissus

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<220>

<221> CDS

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<222> (1) .. (1725)

<223>

<400> 119

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Met Ala Ser Ser Thr Cys Leu Ile His Ser Ser Ser Phe Gly Val Gly
1 5 10 15

10 gga aag aaa gtg aag atg aac acg atg att cga tcg aag ttg ttt tca 96
Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser
20 25 30

15 att cgg tcg gct ttg gac act aag gtg tct gat atg agc gtc aat gct 144
Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
35 40 45

cca aaa gga ttg ttt cca cca gag cct gag cac tac agg ggg cca aag 192
Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
50 55 60

20 ctt aaa gtg gct atc att gga gct ggg ctc gct ggc atg tca act gca 240
Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
65 70 75 80

25 gtg gag ctt ttg gat caa ggg cat gag gtt gac ata tat gaa tcc aga 288
Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg
85 90 95

30 caa ttt att ggt ggt aaa gtc ggt tct ttt gta gat aag cgt gga aac 336
Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn
100 105 110

35 cat att gaa atg gga ctc cat gtg ttt ttt ggt tgc tat aac aat ctt 384
His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu
115 120 125

ttc aga ctt atg aaa aag gta ggt gca gat gaa aat tta ctg gtg aag 432
Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys
130 135 140

40 gat cat act cat acc ttt gta aac cga ggt gga gaa att ggt gaa ctt 480
Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu
145 150 155 160

45 gat ttc cga ctt ccg atg ggt gca cca tta cat ggt att cgt gca ttt 528
Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe

204

	165	170	175	
	cta aca act aat caa ctg aag cct tat gat aaa gca agg aat gct gtg			576
	Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val			
5	180	185	190	
	gct ctt gcc ctt agc cca gtt gta cgt gct ctt att gat cca aat ggt			624
	Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly			
	195	200	205	
10				
	gca atg cag gat ata agg aac tta gat aat att agc ttt tct gat tgg			672
	Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp			
	210	215	220	
15				
	ttc tta tcc aaa ggc ggt acc cgc atg agc atc caa agg atg tgg gat			720
	Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp			
	225	230	235	240
20				
	cca gtt gct tat gcc ctc gga ttt att gac tgt gat aat atc agt gcc			768
	Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala			
	245	250	255	
25				
	cgt tgt atg ctt act ata ttt tct cta ttt gct act aag aca gaa gct			816
	Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala			
	260	265	270	
30				
	tct ctg ttg cgt atg ttg aag ggt tcg cct gat gtt tac tta agc ggt			864
	Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly			
	275	280	285	
35				
	cct ata aga aag tat att aca gat aaa ggt gga agg ttt cac cta agg			912
	Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg			
	290	295	300	
40				
	tgg ggg tgt aga gag ata ctt tat gat gaa cta tca aat ggc gac aca			960
	Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr			
	305	310	315	320
45				
	tat atc aca ggc att gca atg tcg aag gct acc aat aaa aaa ctt gtg			1008
	Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val			
	325	330	335	
50				
	aaa gct gac gtg tat gtt gca gca tgt gat gtt cct gga ata aaa agg			1056
	Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg			
	340	345	350	

	ttg atc cca tcg gag tgg aga gaa tgg gat cta ttt gac aat atc tat Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr 355 360 365	1104
5	aaa cta gtt gga gtt cca gtt gtc act gtt cag ctt agg tac aat ggt Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly 370 375 380	1152
10	tgg gtg aca gag atg caa gat ctg gaa aaa tca agg cag ttg aga gct Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala 385 390 395 400	1200
15	gca gta gga ttg gat aat ctt ctt tat act cca gat gca gac ttt tct Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser 405 410 415	1248
20	tgt ttt tct gat ctt gca ctc tcg tcg cct gaa gat tat tat att gaa Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu 420 425 430	1296
25	gga caa ggg tcc cta ata cag gct gtt ctc acg cca ggg gat cca tac Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr 435 440 445	1344
	atg ccc cta cct aat gat gca att ata gaa aga gtt cgg aaa cag gtt Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val 450 455 460	1392
30	ttg gat tta ttc cca tcc tct caa ggc ctg gaa gtt cta tgg tct tcg Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser 465 470 475 480	1440
35	gtg gtt aaa atc gga caa tcc cta tat cgg gag ggg cct gga aag gac Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp 485 490 495	1488
40	cca ttc aga cct gat cag aag aca cca gta aaa aat ttc ttc ctt gca Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala 500 505 510	1536
45	ggg tca tac acc aaa cag gat tac att gac agt atg gaa gga gcg acc Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr 515 520 525	1584

206

cta tcg ggg aga caa gca gct gca tat atc tgc agc gcc ggt gaa gat 1632
 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

5 ctg gca gca ctt cgc aag aag atc gct gct gat cat cca gag caa ctg 1680
 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

10 atc aac aaa gat tct aac gtg tcg gat gaa ctg agt ctc gta taa 1725
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15 <211> 574

<212> PRT

20 <213> Narcissus pseudonarcissus

<400> 120

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 20 25 30

Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
 35 35 40 45

Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
 50 55 60

40 Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
 65 70 75 80

45

207

	Val	Glu	Leu	Leu	Asp	Gln	Gly	His	Glu	Val	Asp	Ile	Tyr	Glu	Ser	Arg	
					85					90						95	
5	Gln	Phe	Ile	Gly	Gly	Lys	Val	Gly	Ser	Phe	Val	Asp	Lys	Arg	Gly	Asn	
				100					105						110		
10	His	Ile	Glu	Met	Gly	Leu	His	Val	Phe	Phe	Gly	Cys	Tyr	Asn	Asn	Leu	
				115					120						125		
15	Phe	Arg	Leu	Met	Lys	Lys	Val	Gly	Ala	Asp	Glu	Asn	Leu	Leu	Val	Lys	
				130				135						140			
20	Asp	His	Thr	His	Thr	Phe	Val	Asn	Arg	Gly	Gly	Glu	Ile	Gly	Glu	Leu	
				145				150				155				160	
25	Asp	Phe	Arg	Leu	Pro	Met	Gly	Ala	Pro	Leu	His	Gly	Ile	Arg	Ala	Phe	
					165					170					175		
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				180						185					190		
35	Ala	Leu	Ala	Leu	Ser	Pro	Val	Val	Arg	Ala	Leu	Ile	Asp	Pro	Asn	Gly	
				195					200					205			
40	Ala	Met	Gln	Asp	Ile	Arg	Asn	Leu	Asp	Asn	Ile	Ser	Phe	Ser	Asp	Trp	
				210				215					220				
45	Phe	Leu	Ser	Lys	Gly	Gly	Thr	Arg	Met	Ser	Ile	Gln	Arg	Met	Trp	Asp	
				225			230				235				240		
50	Pro	Val	Ala	Tyr	Ala	Leu	Gly	Phe	Ile	Asp	Cys	Asp	Asn	Ile	Ser	Ala	
				245						250					255		
55	Arg	Cys	Met	Leu	Thr	Ile	Phe	Ser	Leu	Phe	Ala	Thr	Lys	Thr	Glu	Ala	

	260	265	270
5	Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly		
	275	280	285
10	Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg		
	290	295	300
15	Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr		
	305	310	315 320
20	Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val		
	325	330	335
25	Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg		
	340	345	350
30	Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr		
	355	360	365
35	Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly		
	370	375	380
40	Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala		
	385	390	395 400
45	Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser		
	405	410	415
50	Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu		
	420	425	430
55	Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr		
	435	440	445

5 Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val
 450 455 460

10 Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser
 465 470 475 480

15 Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp
 485 490 495

20 Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525

25 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

30 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
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35 Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val
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40 <210> 121
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<223>

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15

tgc aag act gta gct ttg ggt gat agc aaa cca aga tac aat aaa cag 96
 Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
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20

aga agt tct tgt ttt gac cct ttg ata att gga aat tgt act gat cag 144
 Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln
 35 40 45

25

cag cag ctt tgt ggc ttg agt tgg ggg gtg gac aag gct aag gga aga 192
 Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg
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aga ggg ggt act gtt tcc aat ttg aaa gca gtt gta gat gta gac aaa 240
 Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys
 65 70 75 80

35

aga gtg gag agc tat ggc agt agt gat gta gaa gga aat gag agt ggc 288
 Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly
 85 90 95

agc tat gat gcc att gtt ata ggt tca gga ata ggt gga ttg gtg gca 336
 Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala
 100 105 110

40

gcg acg cag ctg gcg gtt aag gga gct aag gtt tta gtt ctg gag aag 384
 Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys
 115 120 125

45

tat gtt att cct ggt gga agc tct ggc ttt tac gag agg gat ggt tat 432
 Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr

211

	130	135	140	
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	Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly			
5	145	150	155	160
	aac ctc aat tta att act caa gca ttg gca gca gta gga cgt aaa tta			528
	Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu			
		165	170	175
10				
	gaa gtt ata cct gac cca aca act gta cat ttc cac ctg cca aat gac			576
	Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp			
		180	185	190
15				
	ctt tct gtt cgt ata cac cga gag tat gat gac ttc att gaa gag ctt			624
	Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu			
		195	200	205
	gtg agt aaa ttt cca cat gaa aag gaa ggg att atc aaa ttt tac agt			672
20	Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser			
		210	215	220
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	Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser			
25	225	230	235	240
	ttg gag gaa ccc atc tac ctt ttt ggc cag ttc ttt aag aag ccc ctt			768
	Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu			
		245	250	255
30				
	gaa tgc ttg act ctt gcc tac tat ttg ccc cag aat gct ggt agc atc			816
	Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile			
		260	265	270
35				
	gct cgg aag tat ata aga gat cct ggg ttg ctg tct ttt ata gat gca			864
	Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala			
		275	280	285
	gag tgc ttt atc gtg agt aca gtt aat gca tta caa aca cca atg atc			912
40	Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile			
		290	295	300
	aat gca agc atg gtt cta tgt gac aga cat ttt ggc gga atc aac tac			960
	Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr			
45	305	310	315	320

	ccc gtt ggt gga gtt ggc gag atc gcc aaa tcc tta gca aaa ggc ttg	1008
	Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu	
	325 330 335	
5		
	gat gat cac gga agt cag ata ctt tat agg gca aat gtt aca agt atc	1056
	Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile	
	340 345 350	
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	att ttg gac aat ggc aaa gct gtg gga gtg aag ctt tct gac ggg agg	1104
	Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg	
	355 360 365	
	aag ttt tat gct aaa acc ata gta tcg aat gct acc aga tgg gat act	1152
15	Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr	
	370 375 380	
	ttt gga aag ctt tta aaa gct gag aat ctg cca aaa gaa gaa gaa aat	1200
	Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn	
20	385 390 395 400	
	ttc cag aaa gct tat gta aaa gca cct tct ttt ctt tct att cat atg	1248
	Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met	
	405 410 415	
25		
	gga gtt aaa gca gat gta ctc cca cca gac aca gat tgt cac cat ttt	1296
	Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe	
	420 425 430	
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	gtc ctc gag gat gat tgg aca aat ttg gag aaa cca tat gga agt ata	1344
	Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile	
	435 440 445	
	ttc ttg agt att cca aca gtt ctt gat tcc tca ttg gcc cca gaa gga	1392
35	Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly	
	450 455 460	
	cac cat att ctt cac att ttt aca aca tcg agc att gaa gat tgg gag	1440
	His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu	
40	465 470 475 480	
	gga ctc tct ccg aaa gac tat gaa gcg aag aaa gag gtt gtt gct gaa	1488
	Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu	
	485 490 495	
45		

213

	agg att ata agc aga ctt gaa aaa aca ctc ttc cca ggg ctt aag tca	1536
	Arg Ile, Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser	
	500 505 510	
5	tct att ctc ttt aag gag gtg gga act cca aag acc cac aga cga tac	1584
	Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr	
	515 520 525	
10	ctt gct cgt gat agt ggt acc tat gga cca atg cca cgc gga aca cct	1632
	Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro	
	530 535 540	
15	aag gga ctc ctg gga atg cct ttc aat acc act gct ata gat ggt cta	1680
	Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu	
	545 550 555 560	
20	tat tgt gtt ggc gat agt tgc ttc cca gga caa ggt gtt ata gct gta	1728
	Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val	
	565 570 575	
	gcc ttt tca gga gta atg tgc gct cat cgt gtt gca gct gac tta ggg	1776
	Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly	
	580 585 590	
25	ttt gaa aaa aaa tca gat gtg ctg gac agt gct ctt ctt aga cta ctt	1824
	Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu	
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30	ggt tgg tta agg aca cta gca tga	1848
	Gly Trp Leu Arg Thr Leu Ala	
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35	<210> 122	
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				20					25					30		
10	Arg	Ser	Ser	Cys	Phe	Asp	Pro	Leu	Ile	Ile	Gly	Asn	Cys	Thr	Asp	Gln
				35					40					45		
15	Gln	Gln	Leu	Cys	Gly	Leu	Ser	Trp	Gly	Val	Asp	Lys	Ala	Lys	Gly	Arg
		50					55					60				
20	Arg	Gly	Gly	Thr	Val	Ser	Asn	Leu	Lys	Ala	Val	Val	Asp	Val	Asp	Lys
		65				70					75					80
25	Arg	Val	Glu	Ser	Tyr	Gly	Ser	Ser	Asp	Val	Glu	Gly	Asn	Glu	Ser	Gly
					85					90					95	
30	Ser	Tyr	Asp	Ala	Ile	Val	Ile	Gly	Ser	Gly	Ile	Gly	Gly	Leu	Val	Ala
				100					105					110		
35	Ala	Thr	Gln	Leu	Ala	Val	Lys	Gly	Ala	Lys	Val	Leu	Val	Leu	Glu	Lys
				115					120					125		
40	Tyr	Val	Ile	Pro	Gly	Gly	Ser	Ser	Gly	Phe	Tyr	Glu	Arg	Asp	Gly	Tyr
		130						135					140			
45	Lys	Phe	Asp	Val	Gly	Ser	Ser	Val	Met	Phe	Gly	Phe	Ser	Asp	Lys	Gly
		145					150				155				160	
50	Asn	Leu	Asn	Leu	Ile	Thr	Gln	Ala	Leu	Ala	Ala	Val	Gly	Arg	Lys	Leu
					165					170					175	
55	Glu	Val	Ile	Pro	Asp	Pro	Thr	Thr	Val	His	Phe	His	Leu	Pro	Asn	Asp

215

	180	185	190
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10	Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser 210 215 220		
15	Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser 225 230 235 240		
20	Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu 245 250 255		
25	Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile 260 265 270		
30	Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala 275 280 285		
35	Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile 290 295 300		
40	Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr 305 310 315 320		
45	Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu 325 330 335		
50	Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile 340 345 350		
55	Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg 355 360 365		

Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr
 370 375 380

5

Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn
 385 390 395 400

10

Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met
 405 410 415

15

Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe
 420 425 430

20

Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile
 435 440 445

25

Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly
 450 455 460

30

His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu
 465 470 475 480

Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu
 485 490 495

35

Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser
 500 505 510

40

Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr
 515 520 525

45

Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro
 530 535 540

Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu
 545 550 555 560

5 Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val
 565 570 575

10 Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly
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15 Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu
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20 Gly Trp Leu Arg Thr Leu Ala
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<211> 1233

25 <212> DNA

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<220>

<221> CDS

35 <222> (1)..(1233)

<223>

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	20 25 30	
5	tca tct tct cat tcc cct aac cct cgc cga cac cgc cgc tcc gcc gta	144
	Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val	
	35 40 45	
10	tgc tgc tct ttc gcc tca ctc gac tct gca aaa atc aaa gtc gtt ggc	192
	Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly	
	50 55 60	
15	gtc ggt ggt ggt ggc aac aat gcc gtt aac cgc atg att ggt agc ggc	240
	Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly	
	65 70 75 80	
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	Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu	
	85 90 95	
25	ctg caa tct gtt gca cat aac cct att caa att ggg gag ctt ttg act	336
	Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr	
	100 105 110	
30	cgt gga tta ggt act ggt ggg aac ccg ctt ttg gga gaa cag gct gcg	384
	Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala	
	115 120 125	
35	gag gag tcg aag gaa gcg att ggg aat gcg ctt aaa ggg tcg gat ctt	432
	Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu	
	130 135 140	
40	gtg ttt ata aca gca ggt atg ggt ggt ggg acg ggt tcg ggt gct gct	480
	Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala	
	145 150 155 160	
45	cca gtt gta gcg cag ata gcg aaa gaa gca ggg tat tta act gtt ggt	528
	Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly	
	165 170 175	
50	gtt gta acg tac cca ttc agc ttt gaa ggc cgt aaa aga tca gta cag	576
	Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln	
	180 185 190	

219

	gcg tta gag gct att gag aag ctg caa aag aac gtt gac aca ctt ata	624
	Ala Leu, Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile	
	195 200 205	
5	gtg att cca aat gac cgt ttg ctg gat att gct gat gaa aac acg cct	672
	Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro	
	210 215 220	
10	ctt cag gat gct ttt ctt ctt gct gat gat gta ctc cgc caa gga gtt	720
	Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val	
	225 230 235 240	
15	caa gga atc tca gat ata att aca ata cct ggg ctg gta aat gtg gac	768
	Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp	
	245 250 255	
20	ttt gca gac gtt aaa gca gtc atg aaa gat tct gga act gca atg ctt	816
	Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu	
	260 265 270	
	ggg gtc ggt gtt tcc tca agt aaa aac cga gct gaa gaa gca gct gaa	864
	Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu	
	275 280 285	
25	caa gca act ctt gct cct ttg att gga tca tca att caa tct gct aca	912
	Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr	
	290 295 300	
30	ggg gtt gtt tat aat att acc gga ggg aag gac ata act cta caa gaa	960
	Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu	
	305 310 315 320	
35	gtc aac, agg gtt tct cag gtg gta aca agt ttg gca gat cca tca gca	1008
	Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala	
	325 330 335	
40	aac att ata ttc ggg gca gtg gta gat gag aga tac aac ggg gag att	1056
	Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile	
	340 345 350	
	cat gtg acc att gtt gct act ggc ttt gcc cag tcg ttt cag aaa tct	1104
	His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser	
	355 360 365	
45	ctt ctt gct gac ccg aaa gga gca aaa ctt gtt gat aga aat caa gaa	1152

220

Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

5 cct aca caa cct ttg act tcc gcg aga tct ttg aca aca cct tct cct 1200
 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

10 gct ccg tct cgg tct agg aaa ctc ttc ttt taa 1233
 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

<210> 124

15 <211> 410

<212> PRT

20 <213> Tagetes erecta

<400> 124

25 Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser
 1 5 10 15

30 Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys
 20 25 30

35 Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

40 Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly
 50 55 60

Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly
 65 70 75 80

45 Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu

5	Leu	Gln	Ser	Val	Ala	His	Asn	Pro	Ile	Gln	Ile	Gly	Glu	Leu	Leu	Thr	100	105	110
10	Arg	Gly	Leu	Gly	Thr	Gly	Gly	Asn	Pro	Leu	Leu	Gly	Glu	Gln	Ala	Ala	115	120	125
15	Glu	Glu	Ser	Lys	Glu	Ala	Ile	Gly	Asn	Ala	Leu	Lys	Gly	Ser	Asp	Leu	130	135	140
20	Val	Phe	Ile	Thr	Ala	Gly	Met	Gly	Gly	Gly	Thr	Gly	Ser	Gly	Ala	Ala	145	150	155
25	Pro	Val	Val	Ala	Gln	Ile	Ala	Lys	Glu	Ala	Gly	Tyr	Leu	Thr	Val	Gly	165	170	175
30	Val	Val	Thr	Tyr	Pro	Phe	Ser	Phe	Glu	Gly	Arg	Lys	Arg	Ser	Val	Gln	180	185	190
35	Ala	Leu	Glu	Ala	Ile	Glu	Lys	Leu	Gln	Lys	Asn	Val	Asp	Thr	Leu	Ile	195	200	205
40	Val	Ile	Pro	Asn	Asp	Arg	Leu	Leu	Asp	Ile	Ala	Asp	Glu	Asn	Thr	Pro	210	215	220
45	Leu	Gln	Asp	Ala	Phe	Leu	Leu	Ala	Asp	Asp	Val	Leu	Arg	Gln	Gly	Val	225	230	235
50	Gln	Gly	Ile	Ser	Asp	Ile	Ile	Thr	Ile	Pro	Gly	Leu	Val	Asn	Val	Asp	245	250	255
55	Phe	Ala	Asp	Val	Lys	Ala	Val	Met	Lys	Asp	Ser	Gly	Thr	Ala	Met	Leu	260	265	270

5 Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu
275 280 285

Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr
290 295 300

10 Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu
305 310 315 320

15 Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
325 330 335

20 Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile
340 345 350

25 His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
355 360 365

30 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
370 375 380

Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
385 390 395 400

35 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
405 410

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<211> 891
<212> DNA

<213> Tagetes erecta

5 <220>

<221> CDS

<222> (1)..(891)

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<223>

15 <400> 125

atg aca tcc ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc 48
 Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
 1 5 10 15

20 act ttc ccc aca ttc aat ccc cta cac aaa acc cta act aaa cca aca 96
 Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
 20 25 30

25 cca aaa ccc tac cca aag cca cca cca att cgc tcc gtc ctt caa tac 144
 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
 35 40 45

30 aat cgc aaa cca gag ctc gcc gga gac act cca cga gtc gtc gca atc 192
 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
 50 55 60

35 gac gcc gac gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa 240
 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
 65 70 75 80

aac cgc gtc aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga 288
 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
 85 90 95

40 ctc gac caa gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg 336
 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
 100 105 110

45 ctt tgt att tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga 384
 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly

224

	115	120	125	
	aaa gct tta gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc			432
	Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys			
5	130	135	140	
	ccg gat ttt ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc			480
	Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe			
10	145	150	155	160
	ata acc gcc att aca ccg gct aac gaa gcc gta tta gtt aca aca cct			528
	Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro			
	165	170	175	
15	gat att act gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa			576
	Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu			
	180	185	190	
	tgt gat gga att agg gat att aaa atg att gtg aac aga gtt aga act			624
20	Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr			
	195	200	205	
	gat ttg ata agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag			672
	Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu			
25	210	215	220	
	atg ttg gga ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att			720
	Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile			
30	225	230	235	240
	cgg agt acg aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act			768
	Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr			
	245	250	255	
35	tta gca gga ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa			816
	Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln			
	260	265	270	
	gat agc atg aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga			864
40	Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly			
	275	280	285	
	ttt ttc tcg ttt ttt gga ggt tag tga			891
	Phe Phe Ser Phe Phe Gly Gly			
45	290	295		

<210> 126

5 <211> 295

<212> PRT

10 <213> Tagetes erecta

<400> 126

15 Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
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20 25 30

25 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
35 40 45

30 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
50 55 60

Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
65 70 75 80

35 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
85 90 95

40 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
100 105 110

45 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
115 120 125

Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
130 135 140

5

Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
145 150 155 160

10

Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
165 170 175

15

Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
180 185 190

20

Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
195 200 205

Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
210 215 220

25

Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
225 230 235 240

30

Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
245 250 255

35

Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
260 265 270

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Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly
275 280 285

Phe Phe Ser Phe Phe Gly Gly
290 295

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<210> 127

<211> 332

5 <212> DNA

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aag ctt gca cga gcc tct ctc tat ttt tac act tca atg gcg gca gca 48
 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

25

att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

30

tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

35

ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

40

gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

45

228

atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac 332
 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

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<210> 128

<211> 110

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<212> PRT

<213> Tagetes erecta

15

<400> 128

Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

20

Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

25

Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

30

Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

35

Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

40

Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

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<210> 129
<211> 37
5 <212> DNA
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gcgcatgcat ctagaaatga tccagttaga acaacca
25 <210> 130
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30 <213> Artificial sequence
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37

230

gcgc atgctc tagactat ttt tgctttgtaa atttctg

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<210> 131

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<212> DNA

10 <213> Nostoc punctiforme ATCC 29133

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 Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln
 1 5 10 15

30 gca aaa ctg act cca gta ctg aga agt aaa tct cag ttt aag ggg ctt 97
 Ala Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu
 20 25 30

35 ttc att gct att gtc att gtt agc gca tgg gtc att agc ctg agt tta 145
 Phe Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu
 35 40 45

40 tta ctt tcc ctt gac atc tca aag cta aaa ttt tgg atg tta ttg cct 193
 Leu Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro
 50 55 60

gtt ata cta tgg caa aca ttt tta tat acg gga tta ttt att aca tct 241
 Val Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser
 65 70 75

45 cat gat gcc atg cat ggc gta gta ttt ccc caa aac acc aag att aat 289

231

	His	Asp	Ala	Met	His	Gly	Val	Val	Phe	Pro	Gln	Asn	Thr	Lys	Ile	Asn	
	80						85					90					95
5	cat	ttg	att	gga	aca	ttg	acc	cta	tcc	ctt	tat	ggg	ctt	tta	cca	tat	337
	His	Leu	Ile	Gly	Thr	Leu	Thr	Leu	Ser	Leu	Tyr	Gly	Leu	Leu	Pro	Tyr	
					100					105					110		
10	caa	aaa	cta	ttg	aaa	aaa	cat	tgg	tta	cac	cac	cac	aat	cca	gca	agc	385
	Gln	Lys	Leu	Leu	Lys	Lys	His	Trp	Leu	His	His	His	Asn	Pro	Ala	Ser	
					115				120						125		
15	tca	ata	gac	cgg	gat	ttt	cac	aat	ggg	aaa	cac	caa	agt	ttc	ttt	gct	433
	Ser	Ile	Asp	Pro	Asp	Phe	His	Asn	Gly	Lys	His	Gln	Ser	Phe	Phe	Ala	
			130					135					140				
20	tgg	tat	ttt	cat	ttt	atg	aaa	ggg	tac	tgg	agt	tgg	ggg	caa	ata	att	481
	Trp	Tyr	Phe	His	Phe	Met	Lys	Gly	Tyr	Trp	Ser	Trp	Gly	Gln	Ile	Ile	
			145				150					155					
25	gcg	ttg	act	att	att	tat	aac	ttt	gct	aaa	tac	ata	ctc	cat	atc	cca	529
	Ala	Leu	Thr	Ile	Ile	Tyr	Asn	Phe	Ala	Lys	Tyr	Ile	Leu	His	Ile	Pro	
							165				170				175		
30	agt	gat	aat	cta	act	tac	ttt	tgg	gtg	cta	ccc	tgg	ctt	tta	agt	tca	577
	Ser	Asp	Asn	Leu	Thr	Tyr	Phe	Trp	Val	Leu	Pro	Ser	Leu	Leu	Ser	Ser	
					180					185					190		
35	tta	caa	tta	ttc	tat	ttt	ggg	act	ttt	tta	ccc	cat	agt	gaa	cca	ata	625
	Leu	Gln	Leu	Phe	Tyr	Phe	Gly	Thr	Phe	Leu	Pro	His	Ser	Glu	Pro	Ile	
				195					200					205			
40	ggg	ggg	tat	gtt	cag	cct	cat	tgt	gcc	caa	aca	att	agc	cgt	cct	att	673
	Gly	Gly	Tyr	Val	Gln	Pro	His	Cys	Ala	Gln	Thr	Ile	Ser	Arg	Pro	Ile	
				210				215					220				
45	tgg	tgg	tca	ttt	atc	acg	tgc	tat	cat	ttt	ggc	tac	cac	gag	gaa	cat	721
	Trp	Trp	Ser	Phe	Ile	Thr	Cys	Tyr	His	Phe	Gly	Tyr	His	Glu	Glu	His	
				225			230					235					
50	cac	gaa	tat	cct	cat	att	tct	tgg	tgg	cag	tta	cca	gaa	att	tac	aaa	769
	His	Glu	Tyr	Pro	His	Ile	Ser	Trp	Trp	Gln	Leu	Pro	Glu	Ile	Tyr	Lys	
				240			245			250					255		
55</																	

5 <210> 132
 <211> 257
 <212> PRT
 10 <213> Nostoc punctiforme ATCC 29133
 <400> 132
 15 Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala
 1 5 10 15
 20 Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe
 20 25 30
 Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu
 25 35 40 45
 Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val
 50 55 60
 30
 Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His
 65 70 75 80
 35
 Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His
 85 90 95
 40 Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln
 100 105 110
 45 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Ser
 115 120 125

Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp
 130 135 140
 5
 Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala
 145 150 155 160
 10
 Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser
 165 170 175
 15
 Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu
 180 185 190
 20
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly
 195 200 205
 25
 Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp
 210 215 220
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 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His
 225 230 235 240
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 Lys
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5 <220>

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<222> (1)..(26)

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<223>

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<400> 133

gtcgaccctg ctttaatgag atatgc

26

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<210> 134

<211> 27

<212> DNA

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<213> Artificial sequence

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<222> (1)..(27)

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<223>

<400> 134

40

ctcgagcttg gacaatcagt aaattga

27

<210> 135

<211> 210

<212> DNA

5 <213> Agrobacterium tumefaciens

<220>

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<221> Terminator

<222> (1)..(210)

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<223>

<400> 135

20 gtcgaccctg ctttaatgag atatgcgaga cgccatgat cgcgatgat ttgctttcaa 60

ttctgttgtag caggttgtaa aaaacctgag catgtgtagc tcagatcctt accgccgggt 120

tcggttcatt ctaatgaata tatcaccgt tactatcgta tttttatgaa taatattctc 180

25

cgttcaattt actgattgtc caagctcgag 210

<210> 136

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<211> 37

<212> DNA

35 <213> Artificial sequence

<220>

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<221> Primer

<222> (1)..(37)

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<223>

5 <400> 136
cccgggaatt cttcattatt tcgattttga tttcgtg

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<210> 137

10 <211> 38

<212> DNA

15 <213> Artificial sequence

<220>

20 <221> Primer

<222> (1)..(38)

<223>

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<400> 137
aagcttggtt gatcagaaga agaagaagaa gatgaact

38

30

<210> 138

<211> 652

35

<212> DNA

<213> Arabidopsis thaliana

40

<220>

<221> Promoter

45

<222> (1) .. (652)

<223>

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<400> 138

cccgggaatt cttcattatt tcgattttga tttcgtgacc agcgaacgca gaataccttg 60

10 ttgtgtaata ctttaccgt gtaaatcaaa aacaaaaagg cttttgagct tttttagtt 120

gaatttctct ggctgatctt tctgtacag attcatatat ctgcagagac gatatcattg 180

attatttgag ctctctttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240

15 tgtaaacttt gaagacaaca agaaaggtaa caagtgaggg agggatgact ccatgtcaaa 300

atagatgtca taagaggcgc atcaataagt gcttgagccc attagctagc ccagtaacta 360

20 ccagattgtg agatggatgt gtgaacagtt ttttttttga tgtaggactg aaatgtgaac 420

aacaggcgca tgaaaaggcta aattaggaca atgataagca gaaataactt atcctctcta 480

acacttggcc tcacattgcc cttcacacaa tccacacaca tccaatcaca acctcatcat 540

25 atatctcccg ctaatctttt tttctttgat cttttttttt ttgcttatta tttttttgac 600

tttgatctcc catcagttca tcttcttctt cttcttctga tcaaccaagc tt 652

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<210> 139

<211> 29

35 <212> DNA

<213> Artificial sequence

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<220>

<221> Primer

<222> (1)..(29)

<223>

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<400> 139

gagctctagc gcaatcttat gtggtacaa

29

10

<210> 140

<211> 29

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<212> DNA

<213> Artificial sequence

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<220>

<221> Primer

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<222> (1)..(29)

<223>

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<400> 140

aagcttttct tgaaagtaaa gattgagtc

29

35

<210> 141

<211> 1773

<212> DNA

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<213> Petunia hybrida

<220>

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<223>

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cctacaaatg gttggaggat gggagatttg gctctatcta gagttatgtg gttgttgaag 120

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catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat 180

gacaattacg tgaaagttat ggggtgtttt gtctatcttt gtctaggcct ttcttttcct 240

20

tccaggttgt tgaagatggt ccaattcgat tagaataatg ttttgagctt tagcatattc 300

tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360

tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420

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tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480

actaacatat actagtaaag agaattattaa catggcacat ataatttgat gcaaaatgag 540

30

tatgatgaaa tttaaacccta aaatctcttg attttgacag tgtcaccttg acttggttaac 600

taataagtca tgtttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660

aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat 720

35

ttcaacagga attagttcca cttaactttt aggttacgat acagtgctaa ttaaataact 780

taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840

40

aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg 900

tttgttggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggcaataa 960

tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020

45

ccatttcaca ataaatatcc tagtttgact taaatttagag tttaaaaaat gaaagacgac 1080
 ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140
 5 taacggtaaa gtggtaagtt taaaagttaa ttgttttcaa atataaaatt gtactatcat 1200
 tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc 1260
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 10 tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc 1380
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 15 tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttcga attagtcgag 1500
 cccaaaataa tatatacgtc ggggtggaaaa ctataaaatg tttgacaaaa atgtcaaatt 1560
 aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttacaag 1620
 20 gtagttggtg aagctaagta gcgaatcca ttaccttcca ctctaccta ccccttcac 1680
 caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt tacaagagc 1740
 25 caaagactca atctttactt tcaagaaaag ctt 1773

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30 <211> 39

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40 <221> Primer

<222> (1) .. (39)

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<223>

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<211> 819

35 <212> DNA

<213> Nostoc punctiforme ATCC 29133

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<223>

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<400> 144

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	ggt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg	97
	Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu	
	20 25 30	
15	gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt	145
	Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe	
	35 40 45	
20	tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att	193
	Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile	
	50 55 60	
	gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca	241
25	Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala	
	65 70 75	
	cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat	289
	His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn	
30	80 85 90 95	
	aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat	337
	Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr	
	100 105 110	
35	caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc	385
	Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser	
	115 120 125	
40	gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc	433
	Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe	
	130 135 140	
	tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata	481
45	Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile	

243

	145	150	155	
	gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat			529
	Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His			
5	160	165	170	175
	caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc			577
	Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser			
		180	185	190
10				
	att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag			625
	Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys			
		195	200	205
15				
	aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act			673
	Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr			
		210	215	220
	ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat			721
20	Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His			
		225	230	235
	cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag			769
	His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys			
25	240	245	250	255
	cag aga gta ttc aac aat tca gta acc aat tcg taatctagag catgcgc			819
	Gln Arg Val Phe Asn Asn Ser Val Thr Asn Ser			
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	<211> 266			
35				
	<212> PRT			
	<213> Nostoc punctiforme ATCC 29133			
40				
	<400> 145			
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Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val
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 5

Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu
 35 40 45

10

Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala
 50 55 60

15

Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

20

Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn
 85 90 95

Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln
 100 105 110

25

Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser Glu
 115 120 125

30

Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp
 130 135 140

35

Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val
 145 150 155 160

40

Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln
 165 170 175

Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile
 180 185 190

45

245

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys
195 200 205

5

Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe
210 215 220

10

Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His
225 230 235 240

15

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln
245 250 255

Arg Val Phe Asn Asn Ser Val Thr Asn Ser
260 265

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<210> 146

<211> 33

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<212> DNA

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<220>

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33

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gcgcattgctc tagatcacaa atttgattta ga
25 <210> 148
<211> 720
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30 <213> Nodularia spumigena NSOR10
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<222> (5)..(703)
40 <223>
45 <400> 148

32

247

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	1 5 10 15	
5	agc cta ggt ttg tta ctt tat att gat ata tcc caa ttc aag ttt tgg	97
	Ser Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp	
	20 25 30	
	atg ttg tta ccg ctc ata ttt tgg caa aca ttt tta tat acg gga tta	145
10	Met Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu	
	35 40 45	
	ttt att aca gct cat gat gcc atg cat ggg gta gtt ttt ccc aaa aat	193
	Phe Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn	
15	50 55 60	
	ccc aaa atc aac cat ttc att ggc tca ttg tgc ctg ttt ctt tat ggt	241
	Pro Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly	
	65 70 75	
20	ctt tta cct tat caa aaa ctt tta aaa aag cat tgg cta cat cac cat	289
	Leu Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His	
	80 85 90 95	
25	aat cca gcc agt gaa aca gat cca gat ttt cac aac ggg aag cag aaa	337
	Asn Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys	
	100 105 110	
	aac ttt ttt gct tgg tat tta tat ttt atg aag cgt tac tgg agt tgg	385
30	Asn Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp	
	115 120 125	
	tta caa att atc aca tta atg att att tat aac tta cta aaa tat ata	433
	Leu Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile	
35	130 135 140	
	tgg cat ttt cca gag gat aat atg act tat ttt tgg gta gtt ccc tca	481
	Trp His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser	
	145 150 155	
40	att tta agt tct tta caa tta ttt tat ttt gga act ttt cta ccc cac	529
	Ile Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His	
	160 165 170 175	
45	agt gag cct gta gaa ggt tat aaa gag cct cat cgt tcc caa act att	577

Ser Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile
 180 185 190

5 agc cgt ccc att tgg tgg tca ttt ata act tgt tac cat ttt ggt tat 625
 Ser Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr
 195 200 205

10 cat tac gaa cat cat gaa tac ccc cat gtt cct tgg tgg caa tta cca 673
 His Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro
 210 215 220

15 gaa att tat aaa atg tct aaa tca aat ttg tgatctagag catgcgc 720
 Glu Ile Tyr Lys Met Ser Lys Ser Asn Leu
 225 230

<210> 149

<211> 233

20 <212> PRT

<213> Nodularia spumigena NSOR10

25 <400> 149

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35 Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met
 20 25 30

40 Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe
 35 40 45

45 Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro
 50 55 60

45 Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu

65

70

75

80

5 Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn
85 90 95

10 Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn
100 105 110

15 Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu
115 120 125

Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp
130 135 140

20 His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile
145 150 155 160

25 Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser
165 170 175

30 Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser
180 185 190

35 Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His
195 200 205

Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu
210 215 220

40 Ile Tyr Lys Met Ser Lys Ser Asn Leu
225 230

45 <210> 150

<211> 24

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5 <213> Artificial sequence

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<211> 25

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ctcgagctta cgagcatttt ctaag

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45

<210> 152

<211> 25

<212> DNA

<213> Artificial sequence

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<221> Primer

<222> (1)..(25)

<223>

<400> 152

gaattcccaa taataatcta cagcc

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<210> 153

<211> 25

<212> DNA

<213> Artificial sequence

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<222> (1)..(25)

<223>

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5 <210> 154

<211> 25

<212> DNA

10

<213> Artificial sequence

15 <220>

<221> Primer

<222> (1)..(25)

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<223>

25 <400> 154

gtcgacctct ccattttttc ttcaa

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<210> 155

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<211> 22

<212> DNA

35 <213> Artificial sequence

<220>

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<221> Primer

<222> (1)..(22)

45 <223>

5 <400> 155
gaattcggca cgagcctctc tc

22

<210> 156

10 <211> 23

<212> DNA

15 <213> Artificial sequence

<220>

20 <221> Primer

<222> (1)..(23)

<223>

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<400> 156
ggatcctctc cattttttct tca

23

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<210> 157

<211> 24

35

<212> DNA

<213> Artificial sequence

40

<220>

<221> Primer

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24

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<212> DNA

<213> Artificial sequence

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<220>

<221> Primer

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<222> (1)..(22)

<223>

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<400> 158

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22

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<210> 159

<211> 25

<212> DNA

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<213> Artificial sequence

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<221> Primer

5 <222> (1)..(25)

<223>

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<400> 159

aagcttgcacat ggcggccgga atttc

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15 <210> 160

<211> 307

<212> DNA

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<213> Vicia faba

25 <220>

<221> Terminator

<222> (1)..(307)

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<223> "

35 <400> 160

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atttagaatt gctgtagtca agaacatcag ttctaaaata ttaataaagt tatggccttt 120

40 tgacatatgt gtttcgataa aaaaatcaaa ataaattgag atttattcga aatacaatga 180

aagtttgcag atatgagata tgtttctaca aaataataac ttaaaaactca actatatgct 240

aatgtttttc ttggtgtggt tcatagaaaa ttgtatccgt ttcttagaaa atgctcgtaa 300

45

gctcgag

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<210> 161

<211> 1020

<212> DNA

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<213> *Lycopersicon esculentum*

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<220>

<221> misc_feature

<222> (1)..(1020)

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<223> Nucleic acid encoding a β -hydroxylase

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<400> 161

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ataaccggtt tctcagtcca aaatccgcct caaccgcccc gccggttctg ttcttctctc 120

cgtaactcg caattttggc gcaattttgc tgtctagaag aaagccgaga ttggcggttt 180

30

gttttgtgct ggagaaatgag aaattgaata gtactatcga aagtgagagt gaagtaatag 240

aggatcggat acaagtagag attaatgagg agaagagttt agctgccagt tggctggcgg 300

35

agaaattggc gaggaagaaa tcggagaggt ttacttatct tgtggcagct gtgatgtcta 360

gtttggggat tacttctatg gcgattttgg cggtttatta cagattttca tggcaaattg 420

agggtggaga agtgcctttt tctgaaatgt tagctacatt cactctctcg tttggcgctg 480

40

ccgtaggaat ggagtactgg gcgagatggg ctcatagagc actatggcat gcttctttat 540

ggcacatgca cgagtcgcac catagaccaa gagaaggacc ttttgagatg aacgacgttt 600

45

tcgccataac aaatgctggt ccagctatag gtcttctttc ctacggtttc ttccataaag 660

ggatcgtcc c tggcctctgt ttcggcgctg gattggggat cacagtattt gggatggctt 720
 acatgttcgt tcacgatgga ctggttcata agagatttcc cgtagggcct attgccaaacg 780
 5 tgccttactt tcggagggta gctgcagcac atcagcttca tcactcggac aaatttgatg 840
 gtgtcccata tggcttggtt ctaggaccta aggaattgga agaagtagga ggacttgaag 900
 10 agttagaaaa ggaagtcaac cgaaggatta aaatttctaa gggattatta tgatcaaaag 960
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 15 <210> 162
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 <212> DNA
 20 <213> Petunia hybrida

 25 <220>
 <221> Promoter
 <222> (1)..(1802)
 30 <223>

 35 <400> 162
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 40 catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat 180
 gacaattacg tgaaagttat gggttgtttt gtctattttt gtcgaggcct ttcttttcct 240
 tccaggttgt tgaagatggt ccaattcgat tagaataatg ttttgagctt tagcatattc 300
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	tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat	360
	tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg	420
5	tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct	480
	actaacatat actagtaaag agaattattaa catggcacat ataatttgat gcaaaatgag	540
10	tatgatgaaa tttaaaccca aaatctcttg attttgacag tgtcaccttg acttggttaac	600
	taataagtca tgttttagtg gcagaaagac aaactaatcc accaactgta tagcaataaa	660
	aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat	720
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	aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg	900
20	tttggtggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggcaataa	960
	tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct	1020
25	ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac	1080
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30	tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc	1260
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35	tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc	1380
	caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg	1440
	tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttcga attagtcgag	1500
40	cccaaaataa tatatacgtc ggggtggaaaa ctataaaatg ttgacaaaa atgtcaaatt	1560
	aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttacaag	1620
45	gtagttggtg aagctagtca gcgaatccca ttaccttcca ctctacctaa ccccttcac	1680

caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt tacaaagagc 1740
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5 99 1802

<210> 163
10 <211> 332
<212> DNA
15 <213> Tagetes erecta

<220>
20 <221> misc_feature
<222> (1)..(332)

25 <223> β -Hydroxylase sense fragment

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ataacttgct acttcccctt ttctttttct atcaaatcat ttacccaat tgtagggggc 180
35 agaagatgta ctgtttggtt tggtgccggt ggcgacagta atagtaacag taataataat 240
agtgacagta atagtaataa tccgggtctg gatttaaacc cggcggttat gaaccgtaac 300
40 cgtttggttg aagaaaaaat ggagaggtcg ac 332

<210> 164

<211> 332

<212> DNA

5 <213> Tagetes erecta

<220>

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<221> misc_feature

<222> (1)..(332)

15 <223> β -Hydroxylase antisense fragment

<400> 164

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ttgtagctca agaccatttg gcttaggtcg aatgcgggta ctgggtcata aaccacaac 120

cataacttgt cacttcccct tttctttttc tatcaaata tttaccccaa ttgttagggg 180

25 cagaagatgt actgtttggt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240

tagtgacagt aatagtaata atccgggtct ggatttaaac ccggcggtta tgaaccgtaa 300

30 ccgtttggtt gaagaaaaaa tggagaggat cc 332

<210> 165

35 <211> 996

<212> DNA

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<222> (1)..(996)

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<400> 165

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	ttgtcacttc ccttttctt ttctatcaa atcatttacc ccaattgta ggggcagaag	180
15	atgtactgtt tgttttggt cgggtggcg cagtaatagt aacagtaata ataatagta	240
	cagtaatagt aataatccgg gtctggattt aaaccggcg gttatgaacc gtaaccgttt	300
20	ggttgaagaa aaaatggaga ggaaaaatc ggaacgattt acttatcttg ttgcagctat	360
	tatgtctact ttggaatta cttcaatggc gggtatggcg gtttattacc ggtttcatg	420
	gcaaatggag ggtggagaaa ttccttatgt ggagatgtt ggtacatttg ctctctccgt	480
25	tggtgctgcg gtaggaatgg agtattggcg aagatgggct catgaggcac tatggcatgc	540
	ttctttgtgg cacatgcatg agtcacacca taagccacga gaaggtccgt ttgagcttaa	600
30	tgatgtgtt gctataacaa atgcgggtccc ggccattgcg ttgcttagtt atgggttttt	660
	ccacaaaggc ataattccgg gtctttgttt tggggcggga ctgggaatta cgggtgttgg	720
	aatggcgat atgttcgtcc acgacgggct agttcacaga agattccaag tgggtccgat	780
35	tcgaatgtt ccctatcttc gaaggggtgc agcggctcat cagctgcatc acacggaaaa	840
	atttaatggg gttccttatg gcttgttctt gggacctaa gagctagaag aagtgggtgg	900
40	tacggaagaa ttggacaagg agattcaaag aagaattaa ttgtataata atactaaata	960
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cggattccac caccacttg aaaaattgac atgtcacaat gatttcgtat cctagtcttt 180

30

tattatttaa caqtctcaca atcccattac tctacacctc tttcattaag tcaacacacg 240

gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct 300

35 cctttgttct ctttatatat tgggtccaact aaatcaataa gggaaagcat ccttttggtt 360

ggaggaattg ctttcattct cactctttgt gtgttgatca atggactagc taataacaag 420

ttcctcctct atatatttca aaagaatgga acagaaacat aaacgaaaga cagagtacct 480

40

gatgttgatg attcattgtc tgtctggagc tcccaaattgc cttttatgct tacatattca 540

taaccaacaa cggctattaa ttataaacca aaaacacgaa ataagtttgt agcaaagtga 600

45 aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg 660

5 gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagttgg aaaacctaca 720
 aagtacagaa atggatctgg gccttgaagt gggcttttta ttaaagaaaa aaatacatct 780
 ccgttatcaa tcaccatctt cttctatcta caaattaaag aaggtaacaa cagaacgtgg 840
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18

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<213> Lycopersicon esculentum

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48

1

5

10

15

45

266

	aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc	96
	Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro	
	20 25 30	
5	acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt	144
	Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
	35 40 45	
10	aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
	Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
	50 55 60	
15	tct tta gat gtt aac atc tca tgg gtt gat cct aat tgc aat cgg gct	240
	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
	65 70 75 80	
20	caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
	85 90 95	
25	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
	100 105 110	
30	tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
	115 120 125	
35	ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
	130 135 140	
40	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
	145 150 155 160	
45	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser	
	165 170 175	
50	tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
	180 185 190	
55	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624

267

	Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys	
			195					200					205				
	ata	aga	ggg	agt	ttg	gtt	gtg	gat	gca	agt	ggg	ttt	gct	agt	gat	ttt	672
5	Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe	
			210				215					220					
	ata	gag	tat	gac	agg	cca	aga	aac	cat	ggg	tat	caa	att	gct	cat	ggg	720
10	Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly	
			225				230				235					240	
	gtt	tta	gta	gaa	gtt	gat	aat	cat	cca	ttt	gat	ttg	gat	aaa	atg	gtg	768
	Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val	
					245					250					255		
15	ctt	atg	gat	tgg	agg	gat	tct	cat	ttg	ggg	aat	gag	cca	tat	tta	agg	816
	Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg	
				260					265				270				
20	gtg	aat	aat	gct	aaa	gaa	cca	aca	ttc	ttg	tat	gca	atg	cca	ttt	gat	864
	Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp	
				275				280					285				
	aga	gat	ttg	gtt	ttc	ttg	gaa	gag	act	tct	ttg	gtg	agt	cgt	cct	gtt	912
25	Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val	
			290				295					300					
	tta	tcg	tat	atg	gaa	gta	aaa	aga	agg	atg	gtg	gca	aga	tta	agg	cat	960
	Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His	
30			305			310					315			320			
	ttg	ggg	atc	aaa	gtg	aaa	agt	gtt	att	gag	gaa	gag	aaa	tgt	gtg	atc	1008
	Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile	
				325					330				335				
35	cct	atg	gga	gga	cca	ctt	ccg	cgg	att	cct	caa	aat	gtt	atg	gct	att	1056
	Pro	Met	Gly	Gly	Pro	Leu	Pro	Arg	Ile	Pro	Gln	Asn	Val	Met	Ala	Ile	
				340				345					350				
40	ggg	ggg	aat	tca	ggg	ata	gtt	cat	cca	tca	aca	ggg	tac	atg	gtg	gct	1104
	Gly	Gly	Asn	Ser	Gly	Ile	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	
			355				360					365					
	agg	agc	atg	gct	tta	gca	cca	gta	cta	gct	gaa	gcc	atc	gtc	gag	ggg	1152
45	Arg	Ser	Met	Ala	Leu	Ala	Pro	Val	Leu	Ala	Glu	Ala	Ile	Val	Glu	Gly	

268

	370	375	380	
	ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt			1200
	Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val			
5	385	390	395	400
	tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat			1248
	Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr			
	405	410	415	
10	tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg			1296
	Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg			
	420	425	430	
15	aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg			1344
	Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly			
	435	440	445	
	ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg			1392
20	Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu			
	450	455	460	
	tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca			1440
	Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr			
25	465	470	475	480
	aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag			1488
	Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu			
	485	490	495	
30	agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat			1544
	Ser Leu			
35	tttcatattt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact			1604
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<212> PRT

<213> Lycopersicon esculentum

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Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
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Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
 35 40 45

Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
 50 55 60

Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
 65 70 75 80

Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
 85 90 95

Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
 100 105 110

Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
 115 120 125

Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
 130 135 140

45 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro

270

	145		150		155		160									
5	Tyr	Gly	Arg	Val	Ser	Arg	Lys	Lys	Leu	Lys	Leu	Lys	Leu	Leu	Asn	Ser
					165				170						175	
10	Cys	Val	Glu	Asn	Arg	Val	Lys	Phe	Tyr	Lys	Ala	Lys	Val	Trp	Lys	Val
				180					185					190		
15	Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys
				195				200					205			
20	Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe
				210				215				220				
25	Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly
	225					230				235					240	
30	Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val
				245					250						255	
35	Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg
				260					265					270		
40	Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp
		275						280					285			
45	Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val
		290					295					300				
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	305						310				315				320	
55	Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile
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Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
 340 345 350
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 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
 355 360 365
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 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
 370 375 380
 15
 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
 385 390 395 400
 20
 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
 405 410 415
 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
 420 425 430
 25
 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
 435 440 445
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 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
 450 455 460
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 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
 465 470 475 480
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 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
 485 490 495
 Ser Leu

45